Search History

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 05:25:14 ; Search time 28.6667 Seconds
                 (without alignments)
                 902.703 Million cell updates/sec

Title: US-10-705-757-2
Perfect score: 1670
Sequence: 1 MLLSKINSLAHLRRAAPCNDL...........LLPQETAEIHLHSLSPGPSK 313

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 45 summaries

Database :   Issued_Patents_AA:*
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                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1670	100.0	313	2	US-09-237-543-9	Sequence 9, Appli
2	1670	100.0	313	2	US-09-644-450-9	Sequence 9, Appli
3	1657	99.2	313	1	US-08-463-081B-26	Sequence 26, Appl
4	1657	99.2	313	1	US-08-461-379A-26	Sequence 26, Appl
5	1657	99.2	313	2	US-08-462-390B-26	Sequence 26, Appl
6	1657	99.2	313	2	US-08-463-074B-26	Sequence 26, Appl
7	1657	99.2	313	2	US-08-465-585C-26	Sequence 26, Appl
8	1657	99.2	313	2	US-08-652-446-26	Sequence 26, Appl
9	1636	98.0	313	2	US-09-237-543-8	Sequence 8, Appl
10	1636	98.0	313	2	US-09-644-450-8	Sequence 8, Appl
11	1582	94.7	313	2	US-09-237-543-7	Sequence 7, Appli
12	1582	94.7	313	2	US-09-644-450-7	Sequence 7, Appli
13	1296.5	77.6	257	1	US-07-857-224B-41	Sequence 41, Appl
14	1133	67.8	326	2	US-09-237-543-2	Sequence 2, Appl
15	1133	67.8	326	2	US-09-644-450-2	Sequence 2, Appli
16	1128.5	67.6	455	2	US-09-237-543-5	Sequence 5, Appli
17	1128.5	67.6	455	2	US-09-644-450-5	Sequence 5, Appli
18	1105	66.2	323	2	US-09-237-543-6	Sequence 6, Appli
19	1105	66.2	323	2	US-09-644-450-6	Sequence 6, Appli
20	1079.5	64.6	254	2	US-09-237-543-4	Sequence 4, Appli
21	1079.5	64.6	254	2	US-09-644-450-4	Sequence 4, Appli
22	869.5	52.1	311	2	US-10-184-563-2	Sequence 2, Appli
23	869.5	52.1	372	2	US-09-949-016-7140	Sequence 7140, Ap
24	384.5	23.0	256	2	US-09-966-956-74	Sequence 74, Appl
25	376.5	22.5	776	2	US-09-523-849-34	Sequence 34, Appl
26	376	22.5	1101	2	US-09-770-170-8	Sequence 8, Appli
27	370.5	22.2	778	2	US-10-116-326-2	Sequence 2, Appli
28	370.5	22.2	778	2	US-10-003-690-2	Sequence 2, Appli
29	370.5	22.2	778	2	US-1-803-277-2	Sequence 2, Appli
30	368.5	22.1	630	2	US-10-355-975A-38	Sequence 38, Appl
31	368.5	22.1	631	2	US-09-579-664B-11	Sequence 11, Appl
32	368.5	22.1	631	2	US-10-355-975A-11	Sequence 11, Appl
33	367	22.0	1356	2	US-09-770-170-6	Sequence 6, Appli
34	364.5	21.8	256	2	US-09-964-956-72	Sequence 72, Appl
35	362.5	21.7	1323	2	US-09-770-170-2	Sequence 2, Appli
36	359		511	2	US-09-633-328B-4	Sequence 4, Appli
37	358.5	21.5	281	2	US-09-248-796A-20512	Sequence 20512, A
38	358.5	21.5	668	2	US-10-054-579-2	Sequence 2, Appli
39	357.5	21.4	674	2	US-10-930-181-2	Sequence 2, Appli
40	357.5	21.4	674	2	US-10-283-247-2	Sequence 2, Appli
41	357	21.4	512	2	US-10-633-328B-2	Sequence 2, Appli
42	353.5	21.2	674	2	US-10-283-247-7	Sequence 7, Appli
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44	349.5	20.9	722	2	US-10-817-832B-32	Sequence 32, Appli
45	348.5	20.9	722	2	US-09-984-890-4	Sequence 4, Appli

                              ALIGNMENTS

RESULT 1
US-09-237-543-9
; Sequence 9, Application US/0923754A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-237-543-9

Query Match   100.0%; Score 1670; DB 2; Length 313;
Best Local Similarity   100.0%; Pred. No. 7.5e-161;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db   241 PFEHDEEIIRGQVFFQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313

RESULT 2
US-09-644-450-9

; Sequence 9, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-644-450-9

Query Match   100.0%; Score 1670; DB 2; Length 313;
Best Local Similarity   100.0%; Pred. No. 7.5e-161;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGSGFGSVYSGIRVSD 60
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Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313

RESULT 3
US-08-463-081B-26
; Sequence 26, Application US/08463081B
; Patent No. 5871960 5837487
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,081B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: amino acid
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-463-081B-26

Query Match   99.2%; Score 1657; DB 1; Length 313;
Best Local Similarity   99.4%; Pred. No. 1.6e-159;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313

RESULT 4
US-08-461-379A-26
; Sequence 26, Application US/08461379A
; Patent No. 5871961
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; ADDRESSEE: (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; SOFTWARE: Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: & 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700
TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: peptide
STRANDEDNESS: n.a.
TOPOLOGY: n.a.
MOLECULE TYPE: peptide
US-08-461-379A-26

Query Match   99.2%;   Score 1657; DB 1; Length 313;
Best Local Similarity 99.4%;   Pred. No. 1.6e-159;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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Db   1 MLLSKINSLAHLRAACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313
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RESULT 5
US-08-462-390B-26
Sequence 26, Application US/08462390B
Patent No. 5802894
GENERAL INFORMATION:
APPLICANT: Smith, K. A. & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
ADDRESSEE: (B) STREET:One Westlakes-Berwyn
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 27-OCT-1994
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: peptide
STRANDEDNESS: n.a.
TOPOLOGY: n.a.
MOLECULE TYPE: peptide
US-08-462-390B-26

Query Match   99.2%;   Score 1657; DB 1; Length 313;
Best Local Similarity 99.4%;   Pred. No. 1.6e-159;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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Db   1 MLLSKINSLAHLRAACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313
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RESULT 6
US-08-463-074B-26
Sequence 26, Application US/08463074B
Patent No. 6020155
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein, Vector an
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESSEE: (B) STREET: 444 South Flower St. - Suite 190
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:  PatentIn Release #1.0,
SOFTWARE:  Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074B
  FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/104,736
  FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/796,066
  FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
  NAME: Viviana Amzel, Ph. D.
  REGISTRATION NUMBER: 30,930
  REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (213) 622-7700
  TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
  LENGTH: 313 amino acids
  TYPE: peptide
  STRANDEDNESS: n.a.
  TOPOLOGY: n.a.
MOLECULE TYPE: peptide
US-08-463-074B-26
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Query Match   99.2%;   Score 1657; DB 2; Length 313;
Best Local Similarity   99.4%; Pred. No. 1.6e-159;
Matches 311; Conservative   0; Mismatches 2; Indels 0; Gaps 0;

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Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy    301 EIHLHSLSPGPSK  313
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Db    301 EIHLHSLSPGPSK  313
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RESULT 7
US-08-465-585C-26
; Sequence 26, Application US/08465585C
; Patent No. 6027914
GENERAL INFORMATION:
  APPLICANT: Smith, K. A.; & Beadling, C.
  TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
  TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
  NUMBER OF SEQUENCES: 35
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
  ADDRESSEE:      (B) STREET:  444South Flower St. - Suite 190
  CITY: Los Angeles
  STATE: Californiaa
  COUNTRY: USA
  ZIP: 900071
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COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE:  PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/465,585C
  FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: USSN 08/330,108
  FILING DATE: 27-OCT-1994
  APPLICATION NUMBER: USSN 08/104,736
  FILING DATE: 10-AUG-1993
  APPLICATION NUMBER: USSN 07/796,066
  FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
  NAME: Viviana Amzel, Ph. D.
  REGISTRATION NUMBER: 30,930
  REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (213) 622-7700
  TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
  LENGTH: 313 amino acids
  TYPE: peptide
  STRANDEDNESS: n.a.
  TOPOLOGY: n.a.
MOLECULE TYPE: peptide
US-08-465-585C-26
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Query Match   99.2%;   Score 1657; DB 2; Length 313;
Best Local Similarity   99.4%; Pred. No. 1.6e-159;
Matches 311; Conservative   0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60
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Db      1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy    301 EIHLHSLSPGPSK  313
            |||||||||||||
Db    301 EIHLHSLSPGPSK  313
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```
RESULT 8
US-08-652-446-26
; Sequence 26, Application US/08652446
; Patent No. 6057427
GENERAL INFORMATION:
  APPLICANT: Smith, Kendall A. & Beadling, Carol
  TITLE OF INVENTION: Nucleic Acids Encoding CR5
  TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
  TITLE OF INVENTION: Expression Thereof
  NUMBER OF SEQUENCES: 38
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
  ADDRESSEE:      (B) STREET:  444 South Flower St. - Suite 1900
  ADDRESSEE:
```

; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,446
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP App. # 96921319.8
; FILING DATE: 5-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/96/09194
; FILING DATE: 5-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,108
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463,074
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,337
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,390
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,585
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463,081
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,379
; FILING DATE: 5-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/739,523
; FILING DATE: 29-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: FP66 40035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-652-446-26

Query Match   99.2%;   Score 1657; DB 2; Length 313;
Best Local Similarity 99.4%;   Pred. No. 1.6e-159;
Matches 311; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD   60
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Db   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD   60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

RESULT 9
US-09-237-543-8
; Sequence 8, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-8

Query Match   98.0%;   Score 1636; DB 2; Length 313;
Best Local Similarity 97.1%;   Pred. No. 2.1e-157;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD   60
             ||||||||||||| ||:||||||||||||||||||||||||||||||||||||||||||:
Db   1 MLLSKINSLAHLRARACNDLHANKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVAD   60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDFGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDFGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313

RESULT 10
US-09-644-450-8
; Sequence 8, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23

Query Match   99.2%;   Score 1657; DB 2; Length 313;
Best Local Similarity 99.4%;   Pred. No. 1.6e-159;
Matches 311; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD   60
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Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDFGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDFGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVFFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
             |||||||| |||||||||||||||||||||:||||||:||||||||||||||||| ||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-644-450-8

Query Match              98.0%;  Score 1636;  DB 2;  Length 313;
Best Local Similarity    97.1%;  Pred. No. 2.1e-157;
Matches   304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFPGSGVYSGIRVSD 60
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Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSGVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIVKGQVYFRQRQVSSECQHLIRWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGSSK 313


RESULT 11
US-09-237-543-7
; Sequence 7, Application US/0923754343A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-644-450-7

Query Match              94.7%;  Score 1582;  DB 2;  Length 313;
Best Local Similarity    93.9%;  Pred. No. 6.2e-152;
Matches   294; Conservative  10; Mismatches   9; Indels   0; Gaps   0;

Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFPGSGVYSGIRVSD 60
          ||||||||||||||||:||||||||||||||||||||||||||||||||:|||||||||:|
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSGVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db  241 PFEHDEEIVKGQVYFRQRQVSSECQHLIRWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGSSK 313


RESULT 12
US-09-644-450-7
; Sequence 7, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-644-450-7

Query Match              94.7%;  Score 1582;  DB 2;  Length 313;
Best Local Similarity    93.9%;  Pred. No. 6.2e-152;
Matches   294; Conservative  10; Mismatches   9; Indels   0; Gaps   0;

Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFPGSGVYSGIRVSD 60
          ||||||||||||||||:||||||||||||||||||||||||||||||||:|||||||||:|
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSGVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||:||||||||||||||||||||||||:||||
Db  121 ERPEPVQDLFDFITERGALQEEDLARGFFWQVLEAVRHCINCGVLHRDIKDENILIDLSRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          |||||||||:||||||||||||||||||||||:|||||||||||:|||||||:||||||
Db  241 PFEHDEEIVKGQVYFRQRQVSSECQHLIRWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGSSK 313


RESULT 13
US-07-857-224B-41
; Sequence 41, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
```

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; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER TYPE: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: rat
; FEATURE: Protein kinase; Table 8 Column 46
; PUBLICATION INFORMATION:
; AUTHORS:
; AUTHORS: Hanke, S. K.
; AUTHORS: Quinn, A. M.
; AUTHORS: Hunter, T.
; TITLE: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988

US-07-857-224B-41

Query Match            77.6%;
Best Local Similarity  94.2%;   Score 1296.5;  DB 1;  Length 257;
Matches  242;  Conservative  9;  Mismatches  3;  Indels  3;  Gaps  2;

Qy   36  SQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKK   95
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Db    1  SQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGE--NGTRVMEVVLLKK    58

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Qy  156  RHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRY  215
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; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2:
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-237-543-2

Query Match            67.8%;
Best Local Similarity  69.3%;   Score 1133;  DB 2;  Length 326;
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Qy   58  VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS  115
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Db  119  FLIVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV  178

Qy  176  DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM  235
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Qy  236  VCGDIPFEEHDEEIIRGQVFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM--QDV  293
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US-09-644-450-2
; Sequence 2, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 2:
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-644-450-2

Query Match            67.8%;
Best Local Similarity  69.3%;   Score 1133;  DB 2;  Length 326;
Matches  219;  Conservative  35;  Mismatches  52;  Indels  10;  Gaps  7;

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Qy  116  FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI  175
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Db  119  FLIVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV  178
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RESULT 14
US-09-237-543-2
; Sequence 2, Application US/0923754A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
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Qy    236  VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM--QDV   293
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Db    239  VCGDIPFEQDEEILRGRLLFRRRVSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADG  298

Qy    294  LLPQETAEIHLHSLSP  309
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Db    299  GAP-ESCDLRLCTLDP  313
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OM protein - protein search, using sw model

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                    GenCore version 5.1.7
        Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Run on: May 4, 2006, 05:26:13 ; Search time 92.6667 Seconds
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Title: US-10-705-757-2
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Scoring table: BLOSUM62
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
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| 1 | 1670 | 100.0 | 313 | 3 | US-09-971-791-9 | Sequence 9, Appli |
| 2 | 1670 | 100.0 | 313 | 4 | US-10-081-119-18 | Sequence 18, Appl |
| 3 | 1670 | 100.0 | 313 | 4 | US-10-394-322A-52 | Sequence 52, Appl |
| 4 | 1670 | 100.0 | 313 | 4 | US-10-348-081-13 | Sequence 13, Appl |
| 5 | 1670 | 100.0 | 313 | 4 | US-10-664-421-1 | Sequence 1, Appli |
| 6 | 1670 | 100.0 | 313 | 4 | US-10-664-421-150 | Sequence 150, App |
| 7 | 1670 | 100.0 | 313 | 4 | US-10-705-757-2 | Sequence 2, Appli |
| 8 | 1670 | 100.0 | 313 | 4 | US-10-377-268-9 | Sequence 9, Appli |
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| 12 | 1670 | 100.0 | 313 | 5 | US-10-977-087-18 | Sequence 18, Appl |
| 13 | 1670 | 100.0 | 313 | 5 | US-10-941-635-1 | Sequence 1, Appli |
| 14 | 1670 | 100.0 | 313 | 5 | US-10-941-635-152 | Sequence 152, App |
| 15 | 1657 | 99.2 | 313 | 5 | US-10-620-005A-22 | Sequence 22, Appl |
| 16 | 1636 | 98.0 | 313 | 5 | US-09-971-791-8 | Sequence 8, Appli |
| 17 | 1636 | 98.0 | 313 | 4 | US-10-348-081-12 | Sequence 12, Appl |
| 18 | 1636 | 98.0 | 313 | 3 | US-10-705-757-4 | Sequence 4, Appli |
| 19 | 1582 | 94.7 | 313 | 3 | US-09-971-791-7 | Sequence 7, Appli |
| 20 | 1582 | 94.7 | 313 | 4 | US-10-348-081-14 | Sequence 14, Appl |
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| 22 | 1582 | 94.7 | 313 | 3 | US-10-705-757-6 | Sequence 6, Appli |
| 23 | 1582 | 94.7 | 313 | 5 | US-10-377-268-10 | Sequence 10, Appl |
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| 30 | 1133 | 67.8 | 326 | 3 | US-09-971-791-2 | Sequence 2, Appli |
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| 32 | 1133 | 67.8 | 326 | 4 | US-10-664-421-166 | Sequence 166, App |
| 33 | 1133 | 67.8 | 374 | 4 | US-10-618-941-82 | Sequence 82, Appl |
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| 36 | 1129.5 | 67.6 | 326 | 5 | US-10-705-757-11 | Sequence 11, Appl |
| 37 | 1129.5 | 67.6 | 326 | 4 | US-10-377-268-14 | Sequence 14, Appl |
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| 40 | 1128.5 | 67.6 | 455 | 4 | US-10-705-757-9 | Sequence 9, Appli |
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| 42 | 1116 | 66.8 | 325 | 4 | US-09-971-791-6 | Sequence 6, Appli |
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| 44 | 1105 | 66.2 | 323 | 4 | US-10-348-081-11 | Sequence 11, Appl |
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ALIGNMENTS

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US-09-971-791-9
; Sequence 9, Application US/09971791
; Patent No. US2002011520A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES T
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-791-9

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Qy       61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Qy      121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Qy      181 ELKLIDFGSGALLKDTVYTDFDFGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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; Sequence 18, Application US/10081119
; Publication No. US20030045491A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/081,119
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-119-18

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Best Local Similarity   100.0%;  Pred. No. 2.2e-143;
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RESULT 3
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; Sequence 52, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-52

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Qy  301 EIHLHSLSPGPSK 313
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RESULT 4
US-10-348-081-13
; Sequence 13, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: KORN, Marcus
; APPLICANT: MUELLER, Guenter
; APPLICANT: SCHNEIDER, Rudolf
; APPLICANT: TSCHANK, Georg
; TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: DEAV2002/0004 US NP
; CURRENT APPLICATION NUMBER: US/10/348,081
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 13
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-081-13

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Best Local Similarity   100.0%;  Pred. No. 2.2e-143;
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RESULT 5
US-10-664-421-1
Sequence 1, Application US/10664421
Publication No. US20040142864A1
GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
;
; SEQ ID NO 1
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-1

Query Match   100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1   MLLSKINSLAHLRAAPCNDLIHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   MLLSKINSLAHLRAAPCNDLIHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

Qy 61   NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL   120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61   NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL   120

Qy 121   ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121   ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG   180

Qy 181   ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI   240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181   ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI   240

Qy 241   PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241   PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301   EIHLHSLSPGPSK 313
         |||||||||||||
Db 301   EIHLHSLSPGPSK 313

RESULT 6
US-10-664-421-150
Sequence 150, Application US/10664421
Publication No. US20040142864A1
GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
;
; SEQ ID NO 150
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-150

Query Match   100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1   MLLSKINSLAHLRAAPCNDLIHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   MLLSKINSLAHLRAAPCNDLIHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

Qy 61   NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL   120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61   NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL   120

Qy 121   ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121   ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG   180

Qy 181   ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI   240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181   ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI   240

Qy 241   PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241   PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301   EIHLHSLSPGPSK 313
         |||||||||||||
Db 301   EIHLHSLSPGPSK 313

RESULT 7
US-10-705-757-2
Sequence 2, Application US/10705757
Publication No. US20040169942A1
GENERAL INFORMATION:
; APPLICANT: GRUENENTHAL GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCE: 029310.5281BUS
; CURRENT APPLICATION NUMBER: US/10/705,757
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-757-2

Query Match   100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1   MLLSKINSLAHLRAAPCNDLIHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

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Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240

Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313
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RESULT 8
US-10-377-268-9
; Sequence 9, Application US/10377268
; Publication No. US20040171062A1
; GENERAL INFORMATION:
;   APPLICANT: HIRTH, KLAUS-PETER
;   APPLICANT: MILBURN, MICHAEL VANCE
;   TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
;   FILE REFERENCE: 03363/0303
;   CURRENT APPLICATION NUMBER: US/10/377,268
;   CURRENT FILING DATE: 2003-02-28
;   PRIOR APPLICATION NUMBER: 60/437,929
;   PRIOR FILING DATE: 2003-01-02
;   PRIOR APPLICATION NUMBER: 60/360,651
;   PRIOR FILING DATE: 2002-02-28
;   PRIOR APPLICATION NUMBER: 60/411,398
;   PRIOR FILING DATE: 2002-09-16
;   PRIOR APPLICATION NUMBER: 60/412,341
;   PRIOR FILING DATE: 2002-09-20
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-377-268-9

Query Match   100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240

Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313
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RESULT 9
US-10-951-389-18
; Sequence 18, Application US/10951389
; Publication No. US20050058627A1
; GENERAL INFORMATION:
;   APPLICANT: Reinhard, Christoph
;   APPLICANT: Chan, Vivien W.
;   APPLICANT: Jefferson, Anne B.
;   TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
;   TITLE OF INVENTION: Target in Cancer
;   FILE REFERENCE: 16932.002
;   CURRENT APPLICATION NUMBER: US/10/951,389
;   CURRENT FILING DATE: 2004-09-27
;   PRIOR APPLICATION NUMBER: US/10/081,119
;   PRIOR FILING DATE: 2002-02-21
;   PRIOR APPLICATION NUMBER: 60/289,813
;   PRIOR FILING DATE: 2001-02-21
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-389-18

Query Match   100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240

Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313
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RESULT 10
US-10-951-406-18
; Sequence 18, Application US/10951406
; Publication No. US20050059630A1
; GENERAL INFORMATION:
;   APPLICANT: Reinhard, Christoph
;   APPLICANT: Chan, Vivien W.
;   APPLICANT: Jefferson, Anne B.
;   TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
;   TITLE OF INVENTION: Target in Cancer
;   FILE REFERENCE: 16932.002
;   CURRENT APPLICATION NUMBER: US/10/951,406

```
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-406-18

  Query Match          100.0%;  Score 1670;  DB 5;  Length 313;
  Best Local Similarity 100.0%;  Pred. No. 2.2e-143;
  Matches  313;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313


RESULT 11
US-10-951-477-18
; Sequence 18, Application US/10951477
; Publication No. US20050063974A1
; GENERAL INFORMATION:
;  APPLICANT: Reinhard, Christoph
;  APPLICANT: Jefferson, Anne B.
;  APPLICANT: Chan, Vivien W.
;  TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
;  TITLE OF INVENTION: Target in Cancer
;  FILE REFERENCE: 1692.002
;  CURRENT APPLICATION NUMBER: US/10/951,477
;  CURRENT FILING DATE: 2004-09-27
;  PRIOR APPLICATION NUMBER: US/10/081,119
;  PRIOR FILING DATE: 2002-02-21
;  PRIOR APPLICATION NUMBER: 60/289,813
;  PRIOR FILING DATE: 2001-02-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-477-18

  Query Match          100.0%;  Score 1670;  DB 5;  Length 313;
  Best Local Similarity 100.0%;  Pred. No. 2.2e-143;
  Matches  313;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
           |||||||||||||
Db   301 EIHLHSLSPGPSK 313


RESULT 12
US-10-977-087-18
; Sequence 18, Application US/10977087
; Publication No. US20050130926A1
; GENERAL INFORMATION:
;  APPLICANT: Reinhard, Christoph
;  APPLICANT: Jefferson, Anne B.
;  APPLICANT: Chan, Vivien W.
;  APPLICANT: Kaufmann, Joerg
;  APPLICANT: Xin, Hong
;  APPLICANT: Kennedy, Giulia C.
;  APPLICANT: Khoja, Hamiduddin
;  APPLICANT: Shyamala, Venkatakrishna
;  TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS
;  TITLE OF INVENTION: CELLS AND THEIR METHODS OF USE V
;  FILE REFERENCE: 2300-21986
;  CURRENT APPLICATION NUMBER: US/10/977,087
;  CURRENT FILING DATE: 2004-10-28
;  PRIOR APPLICATION NUMBER: 10/081,119
;  PRIOR FILING DATE: 2002-02-21
;  PRIOR APPLICATION NUMBER: 60/271,254
;  PRIOR FILING DATE: 2001-02-21
;  PRIOR APPLICATION NUMBER: 10/360,848
;  PRIOR FILING DATE: 2003-02-06
;  PRIOR APPLICATION NUMBER: 09/570,593
;  PRIOR FILING DATE: 2000-05-12
;  PRIOR APPLICATION NUMBER: 60/134,112
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: 10/763,692
;  PRIOR FILING DATE: 2004-01-22
;  PRIOR APPLICATION NUMBER: 09/626,301
;  PRIOR FILING DATE: 2000-07-25
;  PRIOR APPLICATION NUMBER: 60/148,936
;  PRIOR FILING DATE: 1999-08-13
;  PRIOR APPLICATION NUMBER: 60/145,612
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: 10/698,959
;  PRIOR FILING DATE: 2003-10-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-087-18

  Query Match          100.0%;  Score 1670;  DB 5;  Length 313;
  Best Local Similarity 100.0%;  Pred. No. 2.2e-143;
  Matches  313;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

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Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313
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RESULT 13
US-10-941-635-1
; Sequence 1, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 1
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-941-635-1

Query Match   100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches   313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENIILIDLNRG 180
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Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENIILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313
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RESULT 14
US-10-941-635-152
; Sequence 152, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 152
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
US-10-941-635-152

Query Match   100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches   313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENIILIDLNRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENIILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  181 ELKLIDFGSGALLKDTVYTDFPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

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Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313
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RESULT 15
US-10-620-052A-22
; Sequence 22, Application US/10620052A
; Publication No. US20040126784A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasunichi
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Markovtsov, Vadim
; APPLICANT: Rigel Pharmaceuticals, Inc.

```
; TITLE OF INVENTION: Modulators of Cellular Proliferation
; FILE REFERENCE: 021044-0040100US
; CURRENT APPLICATION NUMBER: US/10/620,052A
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/395,443
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 22
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: PIM1 oncogene serine threonine kinase
US-10-620-052A-22

  Query Match      99.2%;   Score 1657;  DB 4;  Length 313;
  Best Local Similarity   99.4%;   Pred. No. 3.3e-142;
  Matches   311; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Db       1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy      61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db      61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy     121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy     181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy     241 PFEHDEEIIRGQVFFRQRVSSECCQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 PFEHDEEIIRGQVFFRQRVSSECCQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy     301 EIHLHSLSPGPSK 313
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Db     301 EIHLHSLSPGPSK 313

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbn** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbn** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM protein - protein search, using sw model

Copyright (c) 1993 - 2006 Bioacceleration Ltd.

GenCore version 5.1.7

Run on: May 4, 2006, 05:27:44 ; Search time 15.3333 Seconds
                 (without alignments)
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Title: US-10-705-757-2
Perfect score: 1670
Sequence: 1 MLLSKINSLAHLRAAPCNDL..........LLPQETAEIHLHSLSPGPSK 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA_New:*
        1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep1:*
        2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
        3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
        4: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
        5: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
        6: /SIDS5/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
        7: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
        8: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
        9: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1:*
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       12: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB ID	Description
1	1128.5	67.6	455	9	US-10-784-004-373	Sequence 373, Appl
2	869.5	52.1	311	9	US-10-501-841-40	Sequence 40, Appli
3	869.5	52.1	311	11	US-11-103-065-2	Sequence 2, Appli
4	864	51.7	334	8	US-10-511-937-2982	Sequence 2982, Ap
5	864	51.7	334	8	US-10-501-841-32	Sequence 32, Appl
6	384.5	23.0	256	9	US-10-877-346-74	Sequence 74, Appl
7	382.5	22.9	661	8	US-10-505-928-690	Sequence 690, Appl
8	376	22.5	950	9	US-10-501-035-357	Sequence 357, App
9	368.5	22.1	631	11	US-10-241-056-11	Sequence 11, Appl
10	366	21.9	504	11	US-11-087-099-9816	Sequence 9816, Ap
11	364.5	21.8	256	9	US-11-087-346-72	Sequence 72, Appl
12	364.5	21.8	514	11	US-11-113-424-183	Sequence 183, App
13	356	21.3	514	11	US-11-087-099-11500	Sequence 11500, A
14	352	21.1	512	11	US-11-087-099-3997	Sequence 3997, Ap
15	352	21.1	514	11	US-11-087-099-3612	Sequence 3612, Ap
16	348.5	20.9	619	11	US-11-087-099-12402	Sequence 12402, A
17	348.5	20.9	722	9	US-10-784-004-435	Sequence 435, App
18	348.5	20.9	722	9	US-10-784-004-951	Sequence 951, App
19	348	20.8	472	11	US-11-087-099-11838	Sequence 11838, A
20	346	20.7	86	10	US-10-501-841-37	Sequence 37, Appl
21	342.5	20.5	651	9	US-10-770-726-67	Sequence 67, Appl
22	342.5	20.5	651	11	US-11-177-138-10	Sequence 10, Appl
23	342	20.5	464	11	US-11-096-568A-22124	Sequence 22124, A
24	341	20.4	513	11	US-11-087-099-11726	Sequence 11726, A
25	340	20.4	620	11	US-11-087-099-3898	Sequence 3898, Ap
26	339.5	20.3	504	11	US-11-087-099-12331	Sequence 12331, A
27	339	20.3	713	9	US-11-096-561A-881	Sequence 881, App
28	339	20.3	729	9	US-10-995-561-878	Sequence 878, App
29	339	20.3	737	9	US-11-096-561A-880	Sequence 880, App
30	339	20.3	744	9	US-10-995-561-876	Sequence 876, App
31	339	20.3	753	9	US-11-096-568A-877	Sequence 877, App
32	337.5	20.2	689	9	US-10-204-639-17	Sequence 17, Appl
33	336.5	20.1	445	11	US-11-096-568A-32575	Sequence 32575, A
34	336.5	20.1	448	11	US-11-096-568A-18364	Sequence 18364, A
35	333.5	20.0	1518	11	US-11-096-568A-1886	Sequence 1886, Ap
36	332	19.9	439	11	US-11-096-568A-20431	Sequence 20431, A
37	332	19.9	443	11	US-11-096-568A-20430	Sequence 20430, A
38	328.5	19.7	715	9	US-11-096-561A-65	Sequence 65, Appli
39	328	19.6	582	11	US-11-151-601-4	Sequence 4, Appli
40	327	19.6	358	9	US-10-204-639-65	Sequence 6, Appli
41	327	19.6	582	11	US-11-096-568A-20430	Sequence 20430, A
42	326.5	19.6	765	11	US-11-087-099-905	Sequence 905, App
43	325.5	19.5	278	8	US-11-096-568A-32895	Sequence 32895, A
44	325.5	19.5	278	8	US-10-370-959-17	Sequence 17, Appl
45	325.5	19.5	278	9	US-10-370-959-31	Sequence 31, Appl
					US-10-055-877-149	Sequence 149, App

ALIGNMENTS

RESULT 1
US-10-784-004-373
; Sequence 373, Application US/10784004
; Publication No. US20060084066A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec
; TITLE OF INVENTION: Surrogate Markers of Pain
; FILE REFERENCE: 08201.6029-00000
; CURRENT APPLICATION NUMBER: US/10/784,004
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 1251
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 373
; LENGTH: 455
; TYPE: PRT
; ORGANISM: rat
US-10-784-004-373

Query Match   67.6%;   Score 1128.5; DB 9; Length 455;
Best Local Similarity   72.2%;   Pred. No. 2.5e-88;
Matches 213; Conservative 31; Mismatches 44; Indels 7; Gaps 5;

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Db   130 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR 188

Qy   58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVLLKKV--SSGFSGVIRLLDWFERPDS 115
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Db   189 IADGLPVAVKHVVKERVIEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 247

Qy   116 FVLILERPPEVQDLFDFITERGALQEELARSFFWQVLEAVRHCHCNCGVLHRDIKDENILI 175
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Db   248 FLVLLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHCNCGVVHRDIKDENLLV 307

Qy   176 DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
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Qy   236 VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
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Db   368 VCGDIPFEQDEEILRGRLFFRRRVSPECQQIEWCLSLRPSERPSLDQIAAHPWM 422

RESULT 2

US-10-501-841-40
; Sequence 40, Application No. US20060084055A1
; Publication No. US20060084055A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
; TITLE OF INVENTION: and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058-01440?PC
; CURRENT APPLICATION NUMBER: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-501-841-40

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Query Match          52.1%;  Score 869.5;  DB 9;  Length 311;
Best Local Similarity  58.4%;  Pred. No. 1.7e-66;
Matches 167;  Conservative 39;  Mismatches 75;  Indels 5;  Gaps 2;

Qy    28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP 87
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Qy    88 MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR 145
Db    82 LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141

Qy   146 SFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTR 205
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Qy   206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFRQRVSSECQH 265
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Qy   266 LIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETAEIHLHSLSPGP 311
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RESULT 3
US-11-103-065-2
; Sequence 2, Application US/11103065
; Publication No. US20050282189A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel E., Lora, Jose M.
; TITLE OF INVENTION: 2150, Human Protein Kinase Family
; TITLE OF INVENTION: Member and Uses Therefor
; FILE REFERENCE: MPI2001-137P1RNM
; CURRENT APPLICATION NUMBER: US/11/103,065
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: US/10/184,563
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,702
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0

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Query Match          52.1%;  Score 869.5;  DB 9;  Length 311;
Best Local Similarity  58.4%;  Pred. No. 1.7e-66;
Matches 167;  Conservative 39;  Mismatches 75;  Indels 5;  Gaps 2;

Qy    28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP 87
Db    22 GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP 81

Qy    88 MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR 145
Db    82 LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141
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; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-103-065-2

RESULT 4
US-10-511-937-2982
; Sequence 2982, Application US/10511937
; Publication No. US20060088364A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2982
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-511-937-2982

```
Query Match          51.7%;  Score 864;  DB 8;  Length 334;
Best Local Similarity  61.3%;  Pred. No. 5.5e-66;
Matches 163;  Conservative 37;  Mismatches 64;  Indels 2;  Gaps 1;

Qy    28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP 87
Db    22 GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP 81

Qy    88 MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR 145
Db    82 LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141

Qy   146 SFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTR 205
Db   142 CFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTR 201

Qy   206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFRQRVSSECQH 265
Db   202 VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQELEAELHFPAHVSPDCCA 261

Qy   266 LIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETAEIHLHSLSPGP 311
Db   262 LIRRCLAPKPSSRPSLEEILLDPWMQ---TPAEDVPLNPSKGGPAP 304
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```
Qy    146  SFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTR  205
                 ||  :|||  ||||||||||||||||||||||||||||||||||||||||||||
Db    142  CFFGQVVAAIQHCSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTR  201

Qy    206  VYSPPEWIRYHYRHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFRQRVSSECQH  265
                ||||||  ||||  :|||||||||||||||||||||||||||||  :||  ||||
Db    202  VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHPPAHVSPDCCA  261

Qy    266  LIRWCLALRPSDRPTFEEIQNHPWMQ  291
                ||| ||| :|| ||| |||
Db    262  LIRRCLAPKPSSRPSLEEILLDPWMQ  287
```

RESULT 5
US-10-501-841-32

; Sequence 32, Application US/10501841
; Publication No. US20060840055A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
; TITLE OF INVENTION: and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058-01440ZPC
; CURRENT APPLICATION NUMBER: US/10/501,841
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 32
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-841-32

  Query Match   51.7%;   Score 864;   DB 9;   Length 334;
  Best Local Similarity   61.3%;   Pred. No. 5.5e-66;
  Matches 163;   Conservative 37;   Mismatches 64;   Indels 2;   Gaps 1;

```
Qy     28  GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP   87
                 :||  |||||||||||:|||:||||||||||||:||||:|:||||||||||||||
Db     22  GKDREAFEAEYRLGPLLGKGGFGGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP   81

Qy     88  MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR  145
            :|:||:|||    ||||||||||||||||||:||:||||:||||:|||:|:|||||||:
Db     82  LEVALLWKVGAGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR   141

Qy    146  SFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTR  205
                 ||  :|||  ||||||||||||||||||||||||||||||||||||||||||||
Db    142  CFFGQVVAAIQHCSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTR  201

Qy    206  VYSPPEWIRYHYRHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFRQRVSSECQH  265
                ||||||  ||||  :|||||||||||||||||||||||||||||  :||  ||||
Db    202  VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHPPAHVSPDCCA  261

Qy    266  LIRWCLALRPSDRPTFEEIQNHPWMQ  291
                ||| ||| :|| ||| |||
Db    262  LIRRCLAPKPSSRPSLEEILLDPWMQ  287
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RESULT 6
US-10-877-346-74
; Sequence 74, Application US/10877346

; Publication No. US20060014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shinkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 74
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein kinase
; OTHER INFORMATION: domain Consensus Sequence
US-10-877-346-74

  Query Match   23.0%;   Score 384.5;   DB 9;   Length 256;
  Best Local Similarity   37.0%;   Pred. No. 2.5e-25;
  Matches 98;   Conservative 37.0%;   Mismatches 46;   Indels 23;   Gaps 9;

```
Qy     38  YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS   97
            |:||  ||||:| |||:||||||||||||||||||||||||||||||||  |||||||
Db      1  YELGEKLGSGAFGKVYKGKHKDTGEIVAIKILKKRSLSE----------KKKRFLREIQILRRLS   55

Qy     98  SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERG-ALQEELARSFFWQVLEAVR  156
             ||||||||||||||||:|||:|||||||||||||||||| :|:||||  |
Db     56  --HPNIVRLLGVFEEDDHLYLVMEYMEG-GDLFDYLRRNGLLLSEKEAKKIALQILRGLE  112

Qy    157  HCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVY---TDFDGTRVYSPPEWI  213
            :||  |||||||||||||||||:|||||||||||||||  |   :|:||||:|||||
Db    113  YLHSRGIVHRDLKPENILLDEN-GTVKIADFGLARKLESSSYEKLTTFVGTPEYMAPEVL  171

Qy    214  RYHRYHGRSAAVWSLGILLYDMVCGDIPF---EHDEEIIRGQVFFRQRV-------SSECQ  264
            :|: :||  :|||||:||||||  ||||    |  ||  ||| |:: |       |||
Db    172  EGRGYSSK-VDWWSLGVILYELLTGKLPFPGIDPLEELFRIKERPRLRLPLPPNCSEELK  230
```

```
Qy    265 HLIRWCLALRPSDRPTFEEIQNHPWM 289
          |||||||||||  |||:|||||||||
Db    231 DLIKKCLNKDPEKRPTAKEILNHPWM 255
```

RESULT 7
US-10-505-928-690
; Sequence 690, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
;
; SEQ ID NO 690
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-690

Query Match   22.9%; Score 382.5; DB 8; Length 661;
Best Local Similarity   35.0%; Pred. No. 1.2e-24;
Matches 93; Conservative 49; Mismatches 111; Indels 13; Gaps 8;

```
Qy     31 KEPLESQYQVGPLLGSGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEV  90
          |:|:|: :|   |||:| | : || ||:|||||||:||  | |:||  ||:| ||| |:
Db     48 KHNLKHRYELQETLGKGTYGKVKRATERFSGRVVAIKSIRKDKIKDEQDM---VHIRREI  104

Qy     91 VLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQ  150
          |||||||||||||||||| ||  | | || :||||| ||||||||||||||||||||||
Db    105 EIMS--SLNHPIISIYEVFENDKIVIIMEYASK-GELYDYISERRRLSERETRHFFRQ  161

Qy    151 VLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFG--SGALLKDTVTDFDGTRVYSP  209
          ||  |:|||||||||||||||||| | | ||||||||  |||||||| ||||||||||
Db    162 IVSAVHYCHKNGVVHRDLKLENILLDDN-CNIKIADFGLSNLYQKDKFLQTFCCSPLYAS  220

Qy    210 PEWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFE-HDEEIIRGQVF---FRQRVS-SECQ  264
          | |||:|||||||||||||||||||||||||||  :||:||||| |    |||| ||| |
Db    221 PEIVNGRPYRGPEVDSWALGVLLYTLVCGTMPFDGFDHKNLIRQISSGEYREPTQPSDAR  280

Qy    265 HLIRWCLALRPSDRPTFEEIQNHPWM 290
          |||||||||||||||||||||||||
Db    281 GLIRWMLMVNPDRRATIEDIANHWWV 306
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Query Match   22.5%; Score 376; DB 9; Length 950;
Best Local Similarity   32.4%; Pred. No. 6.6e-24;
Matches 89; Conservative 50; Mismatches 114; Indels 22; Gaps 7;

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Qy     38 YQVGPLLGSGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS  97
          ||:|  || |: | ||:|| ||| |||||||:|||  ||  || | ||||| |:|||||
Db     44 YDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQL---DAVNLEKIYREVQIMKMLD  99

Qy     98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH  157
          ||  | :|   :| |||: :|  || ||| || :| |:: ||  |:|||||||| | |
Db    100 --HPHIIKLYQVMETKSMLYLVTEYAKN-GEIFDYLANHGRLNESEARKFWQILSAVDY  156

Qy    158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD-TVYDFDGTRVYSPPEWIRYH  216
          |||||:||||| ||||||| |:| ||||||||| : :|   | |  ||||||||||||
Db    157 CHGRKIVHRDLKAENLLLD-NNMNIKIADFGFGNFFKSGGELLATWCGSPPYAAPEVFEGQ  215

Qy    217 RYHGRSAAVWSLGILLLYDMVCGDIPFEHD------EEIIRGQVFFRQRVSSECQHLIRWC  270
          |||| |||||||||||:|||||||||||  |    |:|||||| ||||   || || |
Db    216 QYEGPQLDIWSMGVVLYVLVCGALPFDGPTLPILRQRVLEGRFRIPYFMSEDCHLIRM  275

Qy    271 LALRPSDRPTFEEIQNHPWM------QDVLLPQE  298
          ||||||||||||||||||||      ||| ||:
Db    276 LVLDPSKRITIAQIKEHKWMLIEVPVQRPVLYPQE  310
```

RESULT 9
US-11-241-056-11
; Sequence 11, Application US/11241056
; Publication No. US20060024807A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-US
; CURRENT APPLICATION NUMBER: US/11/241,056
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/09/980,464
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 11
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-241-056-11

Query Match   22.1%; Score 368.5; DB 11; Length 631;
Best Local Similarity   33.4%; Pred. No. 1.7e-23;
Matches 98; Conservative 46; Mismatches 116; Indels 33; Gaps 9;

```
Qy     22 ATKLAPGKEKEP---------------LESQYQVGPLLGSGSGGFGSVYSGIRVSDNLPV  64
          | | |||:|:|                |:||||:|  || |: | ||:|| ||| |||
Db     24 ARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTYGKVKKA-RESSGRLV  82

Qy     65 AIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVILLERPE  124
          |||:||  ||  || | ||||| |:|||||||||  | :|   :| |||: :|  || |
Db     83 AIKSIRKDKIKDEQDL---LHIRREIMS--SLNHPIIAIHEVFENSSKIVIMEYAS  137

Qy    125 PVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKL  184
          ||| || :| |:: ||  |:|||||||| | ||||||:||||| |||||||| |:| |
Db    138 R-GDLYDYISERPRLSERDARHFRQIVSALHYCHQNGIVHRDLKAENLLLD-GNIKI  195

Qy    185 IDFG-SGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFE  243
          |||| |||||||| ||||||||||||  |||||||| ||||||||||:|||||||||||
Db    196 ADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYRGPEVDSWSLGVLLYILVHGTMPFD  255

Qy    244 HDE------EIIRQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM  290
          ||:      |:||||| ||||||| ||  |||||||||||||||||||||||
Db    256 GQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATLEDVASHWWV  307
```

RESULT 8
US-10-501-035-357
; Sequence 357, Application US/10501035
; Publication No. US20060462249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 357
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-357

Query Match   22.9%; Score 382.5; DB 8; Length 661;
Best Local Similarity   35.0%; Pred. No. 1.2e-24;
Matches 93; Conservative 49; Mismatches 111; Indels 13; Gaps 8;

RESULT 10
US-11-087-099-9816
Sequence 9816, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9816
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Cucumis sativus
US-11-087-099-9816

Query Match   21.9%;
Best Local Similarity   34.4%;
Matches   90; Conservative   51; Mismatches 105; Indels   16; Gaps   8;

Score 366; DB 11; Length 504;
Pred. No. 2.1e-23;

Qy   38 YQVGPLLGSGGFGGSVYSGIRVSDNLPVAIKHVEVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
             |||:||||||||:||:||||||||:|||:|:||||||::||:|||||||||||:||||:
Db   8 YKLGKTLGIGSFGKVKIAEHALTGHKVAIKILNRKIKN---LDMEEKVRREIKILRLFM 64

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
           :|| ||| ||||| ||:||||:|||||:::|:
Db   65 --HPHIIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 121

Qy   158 CHNCGVLHRDIKDENILLIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH 216
           |||||||||||||||:|:||:|||:||||||||:|||:||||:
Db   122 CHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 180

Qy   217 RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI------IRGQVF-FRQRVSSECQHLIRW 269
           ||||||||||||||||||||:||||||||||:   :|| |:||:|| ||:
Db   181 LYAGPEVDVDWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELPS 239

Qy   270 CLAIRPSDRPTFEEIQNHPWMQ 291
           |:|:|||||||||||:||||
Db   240 MLVVDPMKRITIPEIRQHPWFQ 261

RESULT 11
US-10-877-346-72
Sequence 72, Application US/10877346
Publication No. US20060014153A1
GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2001-08-29

; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 72
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Serine/Threonine protein kinase Consensus
; OTHER INFORMATION: Sequence
US-10-877-346-72

Query Match   21.8%;
Best Local Similarity   33.3%;
Matches   89; Conservative   55; Mismatches   96; Indels   27; Gaps   8;

Score 364.5; DB 9; Length 256;
Pred. No. 1.2e-23;

Qy   38 YQVGPLLGSGGFGGSVYSGIRVSDNLPVAIKHVEVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
           |:|| ||||:||| ||: ||||||||:::|:
Db   1 YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKKEKL----KKKKRERILREIKILKKLD 56

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
           :|| ||| ||:||:::|:
Db   57 --HPNIVKLYDVFEDDDKLYLVMEYCEG--GDLFDLLKKRGRLSEDEARFVARQILSALEY 113

Qy   158 CHNCGVLHRDIKDENILLIDLNRGELKLIDFGSGALLKD--TVYTDFDGTRVYSPPEWIRY 215
           |||||||||||||||:|:||:|||:||||||||:|||
Db   114 LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171

Qy   216 HRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIRGQVFFRQ----------RVSSE 262
           |||||||||||||:||||::|||::
Db   172 GKGYGKAVDIWSLGVILYELLTGKPFPGDDQLL---ALFKKIGKPPPPPPPEWKISPE 228

Qy   263 CQHLIRWCLAIRPSDRPTFEEIQNHPW 289
           |:|:||:
Db   229 AKDLIKKLLVKDPEKRLTAEEALEHPF 255

RESULT 12
US-11-113-424-183
Sequence 183, Application US/11113424
Publication No. US20050260713A1
GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: US/11/113,424
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29

```
;       PRIOR APPLICATION NUMBER: 60/307,506
;       PRIOR FILING DATE: 2001-07-24
;       PRIOR APPLICATION NUMBER: 60/322,358
;       PRIOR FILING DATE: 2001-09-14
;       PRIOR APPLICATION NUMBER: 60/294,075
;       PRIOR FILING DATE: 2001-05-29
;       PRIOR APPLICATION NUMBER: 60/288,153
;       PRIOR FILING DATE: 2001-05-02
;       NUMBER OF SEQ ID NOS: 190
;       SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 183
;       LENGTH: 256
;       TYPE: PRT
;       ORGANISM: Artificial Sequence
;       FEATURE:
;       OTHER INFORMATION: Description of Artificial Sequence: consensus
;       OTHER INFORMATION: sequence
US-11-113-424-183

Query Match             21.8%;  Score 364.5; DB 11; Length 256;
Best Local Similarity   33.3%;  Pred. No. 1.2e-23;
Matches   89; Conservative   55; Mismatches   96; Indels   27; Gaps   8;

Qy         38 YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
              :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db          1 YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKEKL----KKKKRERILREIKILKKLD 56

Qy         98 SGFSGVIRLLDWFERPDSFVLLERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
              :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db         57 --HPNIVKLYDVFEDDDKLYIVMEYCEG-GDLFDLLKKRGRLSEDEARFYARQLSALEY 113

Qy        158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD--TVVTDFDGTRVVSPPEWIRY 215
              ::::::::::::::::::::::::::::::::::::::::  ::::::::::::::::::::
Db        114 LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171

Qy        216 HRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFRQ----------RVSSE 262
              :::::::::::::::::::::::::::::::::::::::::::          ::::::
Db        172 GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL---ALFKKIGKPPPPPPPPEWKISPE 228

Qy        263 CQHLIRWCLALRPSDRPTFEEIQNHPW 289
              ::::::::::::::::::::::::::::
Db        229 AKDLIKLLVKDPEKRLTAEEALEHPF 255

RESULT 13
US-11-087-099-11500
;       Sequence 11500, Application US/11087099
;       Publication No. US20060041961A1
;       GENERAL INFORMATION:
;       APPLICANT: Abad, Mark S. et al.
;       TITLE OF INVENTION: Genes and Uses for Plant Improvement
;       FILE REFERENCE: 38-21(53450)B EP
;       CURRENT APPLICATION NUMBER: US/11/087,099
;       CURRENT FILING DATE: 2005-03-22
;       NUMBER OF SEQ ID NOS: 12464
;
; SEQ ID NO 11500
;       LENGTH: 514
;       TYPE: PRT
;       ORGANISM: Lycopersicon esculentum
US-11-087-099-11500

Query Match             21.3%;  Score 356; DB 11; Length 514;
Best Local Similarity   33.2%;  Pred. No. 1.6e-22;
Matches   87; Conservative   54; Mismatches   105; Indels   16; Gaps   8;

Qy         38 YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
              :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db         19 YKLGKTLGIGSFGKVIAEHTLGHKVAVKILNRRKIRN---MDMEEKVRREIKILRLFM 75

Qy         98 SGFSGVIRLLDWFERPDSFVLLERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
              :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db         76 --HPHIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 132
```

Best Local Similarity 32.2%; Pred. No. 3.4e-22;
Matches 84; Conservative 55; Mismatches 108; Indels 14; Gaps 6;

```
Qy   38  YQVGPLLGSGGGFGSSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
             | :.:|.|||||.|.|:.|  |.|:.| :.  |||: |.   ||.|   ||||||||||
Db   19  YKLGKTLGIGSFGKVKIAEHTLLIGHKVAVKILNRKIRN---MDMEEKVSREIKILRLFM 75

Qy   98  SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
             :|.|.|   :||   | |:::||| ||  |||||.|||.|.:||||.:|| |: :
Db   76  HGH--ISRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 132

Qy  158  CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH 216
             ||   ||||||.||.|:  | :: .|||   |:|   |.|  ||||||||||||||||
Db  133  CHINMVVHRDLKPENLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 191

Qy  217  RYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEIIRGQVFFRQRVSSECQHLIRWC 270
             ||||||.|||||||||:: |  |:||||     :: ||.|  .||||||||||||||||
Db  192  LYAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFKKIKGGYITLPSHLSAGARDLIPRM 251

Qy  271  LALRPSDRPTFEEIQNHPWMQ 291
             | :        |||:||||||||
Db  252  LIVDPMKRMTIPEIRLHPWFQ 272
```

Search completed: May 4, 2006, 05:32:56
Job time : 16.333 secs

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                    GenCore version 5.1.7
                    Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:          May  4, 2006, 05:12:40 ; Search time 113.667 Seconds
                                          (without alignments)
                                          1209.902 Million cell updates/sec

Title:           US-10-705-757-2
Perfect score:   1670
Sequence:        1 MLLSKINSLAHLRAAPCNDL.........LLPQETAEIHLHSLSPGPSK 313

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched:        2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters:  2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  A_geneseq_21:*
            1: genesecp1980s:*
            2: genesecp1990s:*
            3: genesecp2000s:*
            4: genesecp2001s:*
            5: genesecp2002s:*
            6: genesecp2003as:*
            7: genesecp2003bs:*
            8: genesecp2004s:*
            9: genesecp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	1670	100.0	313	5	ABP54943	Human Pim
2	1670	100.0	313	5	ABG33017	Human pro
3	1670	100.0	313	6	AAO19788	Human PIM
4	1670	100.0	313	7	ABU61613	Human PIM
5	1670	100.0	313	7	ABR62939	Human ser
6	1670	100.0	313	7	ADE55368	Human Pro
7	1670	100.0	313	7	ADF45083	Human kin
8	1670	100.0	313	8	ADO19690	Human PRO
9	1670	100.0	313	8	ADB88370	Human PIM
10	1670	100.0	313	8	ADP24227	PRO polyp
11	1670	100.0	313	8	ADT07365	Human pro
12	1670	100.0	313	8	ADT14636	human pro
13	1670	100.0	313	9	ADT86782	human Pim
14	1670	100.0	313	9	ADY86782	Human Pin
15	1670	100.0	313	9	AEA89424	Human Pim
16	1670	100.0	313	9	AEB96037	Human PIM
17	1657	99.2	313	2	AAW08139	Human cyt
18	1657	99.2	313	3	AAY87959	Human CR7
19	1657	99.2	313	8	ADI57202	Human PIM
20	1657	99.2	313	8	ADN03170	Human PIM
21	1657	99.2	313	5	ADY85580	Catalytic
22	1636	98.0	313	5	ABG33016	Rat prote
23	1636	98.0	313	7	AAO19789	Rat PIM1
24	1636	98.0	313	9	ABR62938	Rat serin
25	1582	94.7	313	5	ABG33015	Mouse pro
26	1582	94.7	313	5	AAO19790	Murine PI
27	1582	94.7	313	6	ABR62940	Mouse ser
28	1582	94.7	313	7	ADN97347	Murine Pi
29	1582	94.7	313	8	ADR88371	Mus muscu
30	1582	94.7	313	9	AEA19261	Mouse Pim
31	1582	94.7	313	9	AEB96041	House mou
32	1576	94.4	313	9	AEA12263	Mouse Pim
33	1362	81.6	313	8	ADI57241	PIM1 domi
34	1296.5	77.5	257	2	AAY43942	Rat prote
35	1294.5	77.5	254	2	ADK71853	Human kin
36	1255	75.1	233	8	ADT07367	Human pro
37	1140	68.3	323	8	ADR88376	Human pro
38	1135	68.0	302	8	AAY06886	Plant ful
39	1135	68.0	374	8	ADX91611	Plant ful
40	1133	67.8	326	4	AAB29788	Human ser
41	1133	67.8	326	5	AAE23834	Human HKI
42	1133	67.8	326	5	ABG33011	Human ser
43	1133	67.8	326	7	ABR62932	Human cal
44	1133	67.8	326	7	ADJ96625	Human pro
45	1133	67.8	326	8	ADL97960	Human PIM

ALIGNMENTS

```
RESULT 1
ID          ABP54943
AC          ABP54943;
XX
            ABP54943 standard; protein; 313 AA.
XX
DT          13-JAN-2003  (first entry)
XX
DE          Human Piml.
XX
OS          Homo sapiens.
XX
KW          Piml; tyrosine threonine kinase; TTK; protein kinase; enzyme;
KW          mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
KW          human; gene therapy.
XX
OS          Homo sapiens.
XX
PN          WO200268444-A1.
XX
PD          06-SEP-2002.
XX
PF          21-FEB-2002; 2002WO-US005278.
XX
PR          21-FEB-2001; 2001US-0271254P.
XX
PA          (CHIR ) CHIRON CORP.
XX
PI          Reinhard C, Jefferson AB, Chan VW;
XX
DR          WPI; 2002-698650/75.
DR          N-PSDB; ABV73989.
XX
PT          Reducing growth of cancer cells comprises reducing Tyrosine Threonine
PT          Kinase (TTK) activity, useful in diagnosing and treating disorders with
PT          abnormal expression levels and activity of TTK, such as lung, colon,
PT          prostate and ovarian cancer.
XX
PS          Disclosure; Page 80-81; 113pp; English.
XX
CC          The present sequence is the protein sequence of human Piml, a protein
CC          related to tyrosine threonine kinase (TTK, see ABP54938). TTK
CC          polynucleotides and polypeptides of the invention encompass
CC          polynucleotides and polypeptides having sequence similarity or sequence
CC          identity to human TTK and other genes and gene products related to TTK,
CC          such as Piml. The invention is based on the finding that TTK is
CC          differentially expressed in various forms of cancer. It provides methods
CC          for the identification of cancerous cells, especially breast cancer and
CC          colon cancer cells, by detection of expression levels of TTK, as well as
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CC   diagnostic, prognostic and therapeutic methods. These methods can be used
CC   as the basis of rational therapy. Assays for identifying molecules that
CC   modulate the activity of these genes in cancers, as well as methods of
CC   inhibiting tumour growth by inhibiting the activity of TrK are also
CC   provided
XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1670;  DB 5;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 1.4e-154;
Matches  313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy           1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy          61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120

Qy         121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy         181 ELKLIDFGSGALLKDTVVTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ELKLIDFGSGALLKDTVVTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy         241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy         301 EIHLHSLSPGPSK 313
               |||||||||||||
Db         301 EIHLHSLSPGPSK 313


RESULT 2
ABG33017
ID   ABG33017 standard; protein; 313 AA.
XX
AC   ABG33017;
XX
DT   20-DEC-2002  (first entry)
XX
DE   Human protein kinase phosphorylation site.
XX
KW   HKID-1; serine/threonine kinase; cellular proliferative disorder;
KW   differentiative disorder; cancer; haematopoietic disorder;
KW   Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML;
KW   Waldenstrom's macroglobulinaemia; WM; human.
XX
OS   Homo sapiens.
XX
PN   US20021151120-A1.
XX
PD   22-AUG-2002.
XX
PF   04-OCT-2001; 2001US-0971791.
XX
PR   26-JAN-1999;  99US-00237543.
PR   23-AUG-2000;  2000US-0064450.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R,  Rudolph-Owen LA,  Macbeth K;
XX
DR   WPI; 2002-712471/77.
XX
PT   Modulating levels or activity of HKID-1 polypeptides, a member of
PT   serine/threonine kinase superfamily, for treating cancer, by contacting
PT   cell expressing the polypeptide with a modulator of the polypeptide.
XX
```

```
PS   Example 3; Page 40-41; 48pp; English.
XX
CC   The invention describes a method of modulating the level or activity of
CC   human HKID-1 polypeptide, a member of serine/threonine kinase
CC   superfamily. The method involves contacting a cell expressing the
CC   polypeptide or nucleic acid with an agent to modulate the level or
CC   activity of polypeptide, or level of nucleic acid molecule. The method is
CC   useful for modulating the level or activity of HKID-1 polypeptide or
CC   polynucleotide in a subject having or predisposed to having a disorder
CC   involving cancer. Modulating HKID-1 expression or activity is useful for
CC   therapeutic purposes, for treating cellular proliferative and/or
CC   differentiative disorders including cancer or haematopoietic neoplastic
CC   disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
CC   leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
CC   amino acid sequence of a human protein kinase phosphorylation site
XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1670;  DB 5;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 1.4e-154;
Matches  313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy           1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy          61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120

Qy         121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy         181 ELKLIDFGSGALLKDTVVTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ELKLIDFGSGALLKDTVVTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy         241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy         301 EIHLHSLSPGPSK 313
               |||||||||||||
Db         301 EIHLHSLSPGPSK 313


RESULT 3
AAO19788
ID   AAO19788 standard; protein; 313 AA.
XX
AC   AAO19788;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Human PIM1 kinase.
XX
KW   Human; PIM1 kinase; PIM3 kinase; pain; analgesic.
XX
OS   Homo sapiens.
XX
PN   WO200293173-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-EP005234.
XX
PR   11-MAY-2001; 2001DE-01023055.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
PI   Weihe E,  Schaefer MK;
XX
```

DR   WPI; 2003-120715/11.
DR   N-PSDB; AB269186.
XX
PT   Method for identifying analgesics, useful particularly for treating
PT   chronic pain, by screening compounds for interaction with PIM-1 or -3
PT   kinase, or related compounds.
XX
PS   Claim 1; Fig 1B; 97pp; German.
XX
CC   The present invention relates to a method of identifying pain-regulating
CC   compounds, involving screening candidate compounds and compounds for
CC   PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC   useful for treating chronic pain, particularly of neuropathic or
CC   inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC   neurodegenerative diseases). The present sequence is human PIM1 kinase
XX
SQ   Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 6; Length 313;
Best Local Similarity   100.0%;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
           |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 4
ID   ABU61613 standard; protein; 313 AA.
XX
AC   ABU61613;
XX
DT   11-AUG-2003 (first entry)
XX
DE   Human PIM1 protein.
XX
KW   Human; tyrosine threonine kinase; TTK; cancer; cytostatic;
KW   mitotic checkpoint gene; PIM1.
XX
OS   Homo sapiens.
XX
XX
PN   US2003045491-A1.
XX
PD   06-MAR-2003.
XX
PF   21-FEB-2002; 2002US-00081119.
PR   23-FEB-2001; 2001US-0289813P.
XX
PA   (REIN/) REINHARD C.
PA   (JEFF/) JEFFERSON A B.
PA   (CHAN/) CHAN V W.

XX
PI   Reinhard C, Jefferson AB, Chan VW;
XX
DR   WPI; 2003-455566/43.
DR   N-PSDB; ACA62265.
XX
PT   Detecting cancer in a subject, by comparing expression levels of tyrosine
PT   threonine kinase polypeptide or polynucleotide in a subject and a
PT   normal cell, where an increase in the expression level in the test cell
PT   is indicative of cancer.
XX
PS   Disclosure; Page 34-35; 79pp; English.
XX
CC   The invention relates to detecting cancer (other than ovarian cancer) in
CC   a subject, comprising comparing the expression levels of tyrosine
CC   threonine kinase (TTK), a mitotic checkpoint gene) polypeptide or
CC   polynucleotide in a test cell obtained from the subject and in a normal
CC   non-cancer cell, where an increase in the expression level of TTK protein
CC   or nucleic acid in the test cell compared to that in the normal cell,
CC   indicates the presence of cancer other than ovarian cancer. Also included
CC   are reducing growth of a cancerous cell (by contacting a cancerous cell
CC   with an amount of an agent effective to reduce TTK polypeptide activity
CC   in the cell), an assay for identifying a candidate agent that reduces
CC   growth of a cancerous cell (comprising: (i) detecting the activity of a
CC   TTK polypeptide in the presence of a candidate agent; and (ii) comparing
CC   the activity of the TTK polypeptide in the presence of a candidate agent
CC   relative to TTK polypeptide activity in the absence of the candidate
CC   agent), identifying an agent that reduces TTK activity (comprising: (i)
CC   contacting a cancerous cell displaying elevated expression of a TTK-
CC   encoding polynucleotide with a candidate agent; and (ii) determining the
CC   effect of the candidate agent on TTK polypeptide activity) and assessing
CC   the prognosis of a cancerous disease other than ovarian cancer in a
CC   subject (comprising: (i) detecting expression of TTK -encoding
CC   polynucleotide in a test cancer cell of a subject; and (ii) comparing a
CC   level of expression of the polynucleotide in the test cancer
CC   cell with a level of expression of the polynucleotide in a control non-
CC   cancer cell, where the level of expression of TTK in the test cancer cell
CC   relative to the level of expression in the control non-cancer cell is
CC   indicative of the prognosis of the cancerous disease). The methods are
CC   useful for detecting cancer (other than ovarian cancer) in a subject,
CC   reducing growth of cancerous cells, identifying a candidate agent that
CC   reduces growth of a cancerous cell, identifying an agent that reduces TTK
CC   activity and assessing the prognosis of a cancerous disease other than
CC   ovarian cancer. The methods are also useful for determining the ability
CC   of a subject to respond to a particular therapy e.g. as a basis of
CC   rational therapy. The present sequence represents a closely related
CC   protein to human TTK, in this case human PIM1 (not defined)
XX
SQ   Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 7; Length 313;
Best Local Similarity   100.0%;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

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Qy    301 EIHLHSLSPGPSK 313
          |||||||||||||
Db    301 EIHLHSLSPGPSK 313
```

RESULT 5
ABR62939

```
ID   ABR62939 standard; protein; 313 AA.
XX
AC   ABR62939;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human serine/threonine protein kinase PIM-1.
XX
KW   Human; PIM-1; protein kinase; enzyme.
XX
OS   Homo sapiens.
XX
XX
XX
PN   WO200306013O-A2.
XX
PD   24-JUL-2003.
XX
PF   20-JAN-2003; 2003WO-EP000492.
XX
PR   19-JAN-2002; 2002EP-00001401.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Korn M, Mueller G, Schneider R, Tschank G;
XX
DR   WPI; 2003-598536/56.
XX
PT   New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
PT   agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT   treating insulin resistance or type 2 diabetes mellitus.
XX
PS   Example 2; Page 40; 40pp; English.
XX
CC   The present sequence is the protein sequence of the human
CC   serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins
CC   are the paralogues of novel human and murine PIM-3 proteins (see ABR62932
CC   and ABR62933) of the invention, which are therefore expected to be
CC   involved in cancer and cell growth regulation. PIM-3 is also involved in
CC   the development of insulin resistance and type 2 diabetes mellitus. The
CC   invention relates to the use of PIM-3 nucleic acids and proteins in:
CC   screening assays for compounds that modulate insulin resistance or type 2
CC   diabetes mellitus; detection assays for detecting insulin resistance or
CC   type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
CC   forensic biology); predictive medicine (e.g. diagnostic or prognostic
CC   assays, monitoring clinical trials, pharmacogenomics); and for the
CC   preparing a medicament for the treatment of insulin resistance or type 2
CC   diabetes mellitus
SQ   Sequence 313 AA;
```

```
Query Match             100.0%;  Score 1670;  DB 7;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 1.4e-154;
Matches  313; Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

```
Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGPBGSVVSGIRVEL 60
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||| || 
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGPGGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPVMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPVMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQVRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQVRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
          |||||||||||||
Db  301 EIHLHSLSPGPSK 313
```

RESULT 6
ADE55368

```
ID   ADE55368 standard; protein; 313 AA.
XX
AC   ADE55368;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein AAA60089, SEQ ID NO 1183.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO200316475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C, D'urso D, Befort K, Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; AAA60089.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
```

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CC   injury (CCI)) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   the specification data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
CC
SQ   Sequence 313 AA;

  Query Match             100.0%;  Score 1670;  DB 7;  Length 313;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-154;
  Matches 313;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313


RESULT 7
ADF45083
ID   ADF45083 standard; protein; 313 AA.
XX
AC   ADF45083;
XX
DT   12-FEB-2004   (first entry)
XX
DE   Human kinase PIM1.
XX
KW   Human; protein kinase; enzyme; inhibitor; PIM1.
OS   Homo sapiens.
XX
PN   WO200308121O-A2.
XX
PD   02-OCT-2003.
XX
PF   20-MAR-2003; 2003WO-US008725.
XX
PR   21-MAR-2002; 2002US-0366892P.
XX
PA   (SUNE-) SUNESIS PHARM INC.
XX
PI   Prescott JC; Braisted A;
XX
DR   WPI; 2003-865136/80.
XX
PT   Identifying ligand binding to inactive conformation of target protein
PT   kinase (T) comprises contacting the conformation modified (T) which
PT   contains reactive group at binding site, with ligands and detecting
PT   kinase-ligand conjugate formation.
XX
PS   Disclosure; SEQ ID NO 52; 260pp; English.
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CC   The present invention relates to a method for identifying a ligand (L),
CC   which binds to an inactive conformation of target protein kinase (T). The
CC   method involves contacting inactive conformation of (T), which contains
CC   or is modified to contain a reactive group at or near a binding site of
CC   interest, with one or more ligand candidates capable of covalently
CC   bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC   The method is useful for identifying protein kinase inhibitors that
CC   preferentially bind to inactive conformation of a target protein kinase.
CC   The present sequence is a protein kinase which may be modified via an
CC   amino acid substitution, for use in the method of the invention.
XX
SQ   Sequence 313 AA;

  Query Match             100.0%;  Score 1670;  DB 7;  Length 313;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-154;
  Matches 313;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313


RESULT 8
ADO19690
ID   ADO19690 standard; protein; 313 AA.
XX
AC   ADO19690;
XX
DT   12-AUG-2004   (first entry)
XX
DE   Human PRO polypeptide #308.
XX
KW   Human; PRO; immune related disorder; systemic lupus erythematous;
KW   rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW   systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW   autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW   diabetes mellitus; renal disease; demyelinating disease;
KW   central nervous system; peripheral nervous system;
KW   demyelinating polyneuropathy; Guillain-Barre syndrome;
KW   chronic inflammatory demyelinating polyneuropathy.
OS   Homo sapiens.
XX
PN   WO200404336l-A2.
XX
PD   27-MAY-2004.
XX
PF   06-NOV-2003; 2003WO-US035268.
XX
PR   08-NOV-2002; 2002US-0425235P.
XX
PA   (GETH ) GENENTECH INC.
XX
```

PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX
DR N-PSDB; AD019689.
XX
DR WPI; 2004-420067/39.
XX
PT Novel PRO polypeptide e.g. PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthropathy.
XX
PS Claim 7; SEQ ID NO 616; 1731pp; English.
XX
CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
CC invention.
XX
SQ Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 8; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
         |||||||||||||
Db 301 EIHLHSLSPGPSK 313

RESULT 9
ADR88370
ID ADR88370
AC ADR88370
DE ADR88370 standard; protein; 313 AA.
XX
DT 18-NOV-2004 (first entry)
XX
DE Human PIM 1 protein.
XX
KW Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW G-protein coupled receptor; methyl transferase; ligase; PIM; human.
XX
OS Homo sapiens.
XX
PN US2004171062-A1.

XX
PD 02-SEP-2004.
XX
28-FEB-2003; 2003US-00377268.
XX
DR WPI; 2004-642017/62.
XX
PI Hirth K, Milburn MV;
XX
(PLEX-) PLEXXIKON INC.
XX
PT Designing a ligand binding to a target molecule, comprises identifying as
PT molecular scaffolds compounds binding to members of a molecular family,
PT detecting orientation of scaffolds at a binding site of target, and
PT synthesizing ligand.
XX
Disclosure; SEQ ID NO 9; 186pp; English.
XX
CC The present invention relates to a method of designing a ligand binding
CC to a target molecule. The method involves identifying as molecular
CC scaffolds compounds binding to members of a molecular family, detecting
CC orientation of scaffolds at a binding site of target, and synthesising
CC ligand. The invention is useful for designing drug products and for
CC designing ligand binding to target molecules such as nuclear hormone
CC receptors, TNF receptors, G-protein coupled receptor, methyl
CC transferases, ligases, etc. The present sequence is the human PIM 1
CC protein. This sequence is used to illustrate the method of invention.
XX
SQ Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 8; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
         |||||||||||||
Db 301 EIHLHSLSPGPSK 313

RESULT 10
ADP24227
ID ADP24227
AC ADP24227
DE ADP24227 standard; protein; 313 AA.
XX
DT 18-NOV-2004 (first entry)
XX
DE PRO polypeptide SEQ ID NO:1405.

XX
KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX
OS Unidentified.
XX
PN WO200041170-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034312.
XX
PR 01-NOV-2002; 2002US-0423394P.
XX
PA (GETH) GENENTECH INC.
XX
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-419628/39.
DR N-PSDB; ADP24226.
XX
PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
PS Claim 7; SEQ ID NO 1405; 2940pp; English.
XX
CC The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX
SQ Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 8; Length 313;
Best Local Similarity   100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPSGVYSGIRVSD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPSGVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Db
Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKILDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Db   181 ELKILDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
              |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 11
AD T07365
ID ADT07365 standard; protein; 313 AA.
XX
AC ADT07365;
XX
DT 13-JAN-2005 (first entry)
XX
OS Homo sapiens.
XX
PN WO200490158-A1.
XX
PD 21-OCT-2004.
XX
DE Human protein #1 associated to anticancer compound screening method.
XX
KW prophylactic-therapeutic agent; apoptosis inducing agent;
KW anticancer agent; serine/threonine kinase Pim-1; cancer; solid tumour;
KW human.
XX
OS Homo sapiens.
XX
PN WO200490158-A1.
XX
PD 21-OCT-2004.
XX
PF 05-APR-2004; 2004WO-JP004917.
XX
PR 03-APR-2003; 2003US-0459644P.
XX
PA (ONCO-) ONCOREX INC.
XX
PI Kobayashi M, Jian C;
XX
DR WPI; 2004-748778/73.
DR N-PSDB; ADT07366.
XX
PT Screening for a prophylactic-therapeutic apoptosis inducing agent or
PT enhancer of anticancer agent, comprises use of serine/threonine kinase
PT Pim-1, its partial peptide or its salt.
XX
PS Disclosure; SEQ ID NO 1; 93pp; Japanese.
XX
CC The invention relates to a method of screening a prophylactic-therapeutic
CC agent for an apoptosis inducing agent or an enhancer of an anticancer
CC agent. The method involves the use of a serine/threonine kinase Pim-1,
CC its partial peptide or its salt. Also disclosed is a kit for carrying out
CC the method of the invention. The method is useful for screening a
CC prophylactic-therapeutic agent for cancer. The method is also useful for
CC prophylaxis and/or treatment of cancer, inducing apoptosis, treating a
CC patient having a solid tumour that is resistant to an anticancer agent
CC (induced by hypoxia), and for screening a substance that promotes or
CC inhibits the activity of serine/threonine kinase Pim-1. The present
CC sequence represents a human polypeptide relating to the present
CC invention.
XX
SQ Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 8; Length 313;
Best Local Similarity   100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPSGVYSGIRVSD 60

RESULT 12
ADT14636
ID   ADT14636 standard; protein; 313 AA.
XX
AC   ADT14636;
XX
DT   13-JAN-2005 (first entry)
XX
DE   human Pim-1 (oncogene-encoded serine/threonine kinase) protein.
XX
KW   crystallography; Pim-1; cancer; serine/threonine kinase; enzyme;
KW   protein co-ordinate data; protein structure.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   Domain   33..121
FT   /label= Location/Qualifiers
FT   /note = N-terminal domain
FT   Domain   44..52
FT   /note = Glycine-rich loop
FT   Domain   122..127
FT   /note = Hinge region
FT   Domain   128..305
FT   /note = C-terminal domain
FT   Modified-site 166
FT   /label= OTHER
FT   /note= "OTHER = Forms a salt bridge via linkage to
FT   Asp200"
FT   Modified-site 200
FT   /note = Activation loop
FT   /label= OTHER
FT   Domain   186..210
FT   /label= OTHER
FT   /note= "OTHER = Forms a salt bridge via linkage to
FT   Arg166"
XX

Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
Qy   301 EIHLHSLSPGPSK 313
         |||||||||||||
Db   301 EIHLHSLSPGPSK 313

CC   The invention relates to a novel crystal comprising a human Pim-1
CC   (oncogene-encoded serine/threonine kinase) protein, a Pim-1 homologue, a
CC   human Pim-1 protein complex or a Pim-1 homologue complex. Pim-1 is
CC   primarily expressed in haemopoietic and germ cell lines and this
CC   expression is tightly regulated and induced by cytokines, mitogens and
CC   hormones. Human Pim-1 is associated with multiple cellular functions,
CC   such as proliferation, differentiation, apoptosis and tumourigenesis. The
CC   crystal of the invention relates particularly to the residues involved in
CC   the active site and binding sites of Pim-1. Such information may be
CC   useful for developing Pim-1 inhibitors that are useful as therapeutic
CC   agents in the treatment of cancer. The current sequence is that of the
CC   human Pim-1 (oncogene-encoded serine/threonine kinase) protein of the
CC   invention.
XX
SQ   Sequence 313 AA;

XX
PT   Crystal useful for developing Pim-1 (oncogene-encoded serine/threonine
PT   kinase) inhibitors, comprises human Pim-1 protein, Pim-1 protein complex, human
PT   Pim-1 protein complex, or Pim-1 homologue complex.
XX
     Claim 8; SEQ ID NO 2; 219pp; English.

Query Match   100.0%; Score 1670; DB 8; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
Qy   301 EIHLHSLSPGPSK 313
         |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 13
ADY86782
ID   ADY86782 standard; protein; 313 AA.
XX
AC   ADY86782;
XX
DT   02-JUN-2005 (first entry)
XX
DE   Human Pim1 protein, SEQ ID NO: 18.
XX
KW   Prognosis; cancer; cytostatic; neoplasm; tyrosine threonine kinase; TTK;
KW   Pim1.
XX
OS   Homo sapiens.
XX

```
PR   21-FEB-2001; 2001US-0271254P.
PR   23-FEB-2001; 2001US-0289813P.
PR   21-FEB-2002; 2002US-00081119.
XX
PA   (REIN/) REINHARD C.
PA   (JEFF/) JEFFERSON A B.
PA   (CHAN/) CHAN V W.
XX
PI   Reinhard C, Jefferson AB, Chan VW;
XX
DR   WPI; 2005-241248/25.
DR   N-PSDB; ADY86781.
XX
PS   Disclosure; SEQ ID NO 18; 78pp; English.
XX
PT   Assessment of prognosis of a cancerous disease other than ovarian cancer
PT   comprises detection and comparison of expression of a tyrosine threonine
PT   kinase-encoding polynucleotide in a test cancer cell with a control non-
PT   cancer cell.
XX
CC   The invention relates to a method for assessing the prognosis of a
CC   cancerous disease other than ovarian cancer which involves detection and
CC   comparison of expression of a tyrosine threonine kinase (TTK)-encoding
CC   polynucleotide in a test cancer cell with a control non-cancer cell. The
CC   method is useful to assess the prognosis of a cancerous disease other
CC   than ovarian cancer. It is useful to identify cancerous cells and to
CC   determine the ability of a subject to respond to a particular therapy
CC   e.g. as the basis of rational therapy. The present sequence is the TTK
CC   related human Pim1 protein.
XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1670;  DB 9;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 1.4e-154;
Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313


RESULT 14
AEA89424

ID   AEA89424 standard; protein; 313 AA.
XX
AC   AEA89424;
XX
DT   25-AUG-2005  (first entry)
XX
DE   Human Pim1 protein, SEQ ID NO: 18.
XX
KW   Drug screening; diagnosis; therapeutic; cancer; cytostatic; neoplasm;
KW   Pim1.
XX
OS   Homo sapiens.
XX
PN   US2005130926-A1.
XX
PD   16-JUN-2005.
XX
PF   28-OCT-2004; 2004US-00977087.
XX
PR   06-NOV-1998; 98US-0107112P.
PR   06-JAN-1999; 99US-0114856P.
PR   14-MAY-1999; 99US-0134112P.
PR   26-JUL-1999; 99US-0145612P.
PR   13-AUG-1999; 99US-0148936P.
PR   03-NOV-1999; 99US-0433360.
PR   12-MAY-2000; 2000US-0570593.
PR   25-JUL-2000; 2000US-0626301.
PR   21-FEB-2001; 2001US-0271254P.
PR   21-FEB-2002; 2002US-00081119.
PR   06-FEB-2002; 2002US-00360848.
PR   30-OCT-2003; 2003US-00698959.
PR   22-JAN-2004; 2004US-00763692.
XX
DR   WPI; 2005-457024/46.
DR   N-PSDB; AEA89423.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Reinhard C, Jefferson AB, Chan VW, Kaufmann J, Xin H, Kennedy GC;
PI   Harrowe G, Khoja H, Shyamala V;
XX
PS   Disclosure; SEQ ID NO 18; 206pp; English.
XX
PT   New isolated human HX2004-6 polypeptide or isolated VSHK-1 polypeptide,
PT   useful for diagnosing or treating cancer, where VSHK-1 is also used to
PT   identify a VSHK-1 receptor ligand.
XX
CC   The invention relates to human HX2004-6 protein and a seven transmembrane
CC   receptor protein referred as VSHK-1 useful for diagnosing or treating
CC   cancer. The invention also relates to a method for reducing the growth of
CC   a cancerous cell. VSHK-1 is useful for identifying a VSHK-1 receptor
CC   ligand and to identify a substance which modulates its signal
CC   transduction activity. The HX2004-6 DNA is useful to detect the presence
CC   of HX2004-6 in a biological sample (e.g. ductal epithelial cells from
CC   tissue chosen from pancreas, colon and breast). The invention is useful
CC   for screening drugs for the treatment of cancer. The present sequence is
CC   the human Pim1 protein. This sequence is differentially expressed in
CC   cancer cells.
XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1670;  DB 9;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 1.4e-154;
Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  301 EIHLHSLSPGPSK 313
            |||||||||||||
Db  301 EIHLHSLSPGPSK 313


RESULT 15
AEB96037
ID   AEB96037 standard; protein; 313 AA.
XX
AC   AEB96037;
XX
DT   20-OCT-2005  (first entry)
XX
DE   Human PIM-1 serine-threonine kinase protein.
XX
KW   micturition disorder; urinary dysfunction; uropathic; gene therapy;
KW   PIM-1 protein kinase; serine-threonine kinase; enzyme.
OS   Homo sapiens.
XX
PN   DE102004004894-A1.
XX
PD   18-AUG-2005.
XX
PF   30-JAN-2004; 2004DE-10004894.
PR   30-JAN-2004; 2004DE-10004894.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
PI   Christoph T;
XX
DR   WPI; 2005-556609/57.
DR   N-PSDB; AEB96036.
DR   REFSEQ; NP_002639.
XX
PT   Identifying substances that regulate PIM kinases, useful for treatment
PT   and diagnosis of urinary incontinence and the urge to urinate, and
PT   similar use of PIM proteins or nucleic acids.
XX
PS   Claim 1; Fig 1B; 37pp; German.
XX
CC   The invention relates to a novel method for identifying substances that
CC   regulate urinary incontinence and the urge to urinate. The method
CC   comprises incubating a test compound with a cell and/or cell preparation
CC   that has synthesized a specific protein of the PIM (proviral integration
CC   site) kinase family and measuring either binding of the test compound to
CC   the PIM kinase, or a functional parameter that is altered by the binding.
CC   The method of the invention demonstrates uropathic and gene therapy
CC   applications and may be useful for treatment and diagnosis of urinary
CC   incontinence and the urge to urinate. The method is based upon regulating
CC   the activity or expression of PIM kinases that are involved in bladder
CC   control. The current sequence is that of the human PIM-1 serine-threonine
CC   kinase protein of the invention.
XX
SQ   Sequence 313 AA;


Query Match             100.0%;  Score 1670;  DB 9;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 1.4e-154;
Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MLLSKINSLAHLRRAAPCNDLHATKLAPGKEKEPLESQYGVGPLLGSGGFPGSVYSGIRVSD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRRAAPCNDLHATKLAPGKEKEPLESQYGVGPLLGSGGFPGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
          |||||||||||||
Db  301 EIHLHSLSPGPSK 313
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Search completed: May 4, 2006, 05:24:45
Job time : 118.667 secs

OM protein - protein search, using sw model

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GenCore version 5.1.7

Run on: May 4, 2006, 05:19:22 ; Search time 20.3333 Seconds
                 (without alignments)
                 1481.107 Million cell updates/sec

Title: US-10-705-757-2
Perfect score: 1670
Sequence: 1 MLLSKINSLAHIRAAPCNDL.........LLPQETAEIHLHSLSPGPSK 313

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1670	100.0	313	1	TVHUP1	protein kinase (EC
2	1636	98.0	313	1	S26298	protein kinase (EC
3	1582	94.7	313	1	TVMSP1	protein kinase (EC
4	881.5	52.8	370	1	S55333	protein kinase pim
5	617	36.9	363	2	T22255	hypothetical prote
6	486	29.1	409	2	T15435	hypothetical prote
7	386	23.1	481	2	I49072	protein kinase - m
8	380	22.8	1398	2	S13741	hypothetical prote
9	376	22.5	1101	2	S66730	hypothetical prote
10	367	22.0	1358	2	S33653	probable serine/th
11	366	21.9	504	2	T10049	probable serine/th
12	361	21.6	651	2	S55244	p69Eg3 protein - A
13	361	21.6	798	2	JC7500	qik protein - chic
14	360	21.6	512	1	A56009	serine/threonine-s
15	359	21.5	512	1	JC1446	serine/threonine-s
16	357	21.4	511	1	T52653	serine/threonine-s
17	352	21.1	472	2	T07788	SNF-related kinase
18	348	20.8	469	2	B90100	probable serine/th
19	347.5	20.8	887	2	B84644	hypothetical protein
20	347.5	20.8	726	2	T20941	hypothetical protein
21	345	20.7	726	2	T33998	hypothetical prote
22	342.5	20.5	489	2	T04862	probable serine/th
23	342.5	20.5	1558	1	T29253	hypothetical prote
24	341.5	20.4	414	2	JN0323	Ca2+/calmodulin-de
25	341	20.4	513	1	S60304	serine/threonine-s
26	339.5	20.3	504	2	T07415	probable serine/th
27	337	20.2	502	2	T02306	probable serine/th
28	337	20.2	713	2	S27966	probable serine/th
29	336.5	20.1	445	2	T50802	serine/threonine p
30	335	20.1	745	2	G01025	serine/threonine p
31	333.5	20.0	1518	2	S37928	probable purine nu
32	331.5	19.9	774	2	I48609	probable serine/th
33	331	19.8	435	2	E84707	probable protein k
34	330.5	19.8	339	2	S56719	serine/threonine-s
35	330.5	19.8	520	2	G86414	probable protein k
36	330.5	19.8	553	1	T02139	calcium-dependent
37	328	19.6	591	2	S54788	calcium-stimulated
38	327	19.6	582	2	B84721	calcium-dependent
39	326.5	19.6	746	2	S62365	probable calcium-d
40	325.5	19.5	442	2	T48203	SNF1-related prote
41	325	19.5	1246	2	G89287	protein H3E23.1 [
42	324.5	19.4	713	2	T37886	probable serine/th
43	324	19.4	401	2	B90120	SNF1-related prote
44	323	19.3	461	2	T14822	probable serine/th
45	323	19.3	473	1	S59941	serine/threonine-s

ALIGNMENTS

RESULT 1
TVHUP1
protein kinase (EC 2.7.1.37) pim-1 - human
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene pro
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JU0327; A46554; A27476; 158412
R;Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.
Gene 90, 303-307, 1990
A;Molecule type: DNA
A;Residues: 1-313 <REE>
A;Cross-references: UNIPROT:P11309; UNIPARC:UPI000000001060; GB:M27903; NID:g189958; PID
A;Title: Primary structure of the putative human oncogene, pim-1.
A;Reference number: JU0327; MUID:90382681; PMID:2205533
A;Accession: JU0327
A;Molecule type: DNA
A;Residues: 1-313 <REE>
A;Cross-references: UNIPARC:UPI000000001060; GB:M24779; NID:g1066790; PIDN:AAA81553.1; P
R;Zakut-Houri, R.; Hazum, S.; Givol, D.; Telerman, A.
Gene 54, 105-111, 1987
A;Title: The cDNA sequence and gene analysis of the human pim oncogene.
A;Reference number: A27476; MUID:87277423; PMID:3475233
A;Accession: A27476
A;Molecule type: mRNA
A;Residues: 1-14, 'RA', 17-313 <ZAK>
A;Cross-references: UNIPARC:UPI000014987C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PI
R;Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.
Oncogene Res. 1, 103-112, 1987
A;Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immuno
A;Reference number: 158412; MUID:88217305; PMID:3329709
A;Accession: 158412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-313 <DOM>
A;Cross-references: UNIPARC:UPI000000001060; GB:M54915; NID:g189961; PIDN:AAA36447.1; PI
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
A;Gene: GDB:PIM1
A;Cross-references: GDB:119495; OMIM:164960
A;Map position: 6p21.2-6p21.2
A;Introns: 28/2; 63/3; 80/3; 203/1; 262/1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncoge
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif

F;67/Active site: Lys #status predicted

```
Query Match            100.0%;  Score 1670;  DB 1;  Length 313;
Best Local Similarity  100.0%;  Pred. No. 1.9e-76;
Matches 313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy    301 EIHLHSLSPGPSK 313
          |||||||||||||
Db    301 EIHLHSLSPGPSK 313
```

RESULT 2
S26298
protein kinase (EC 2.7.1.37) pim-1 - rat
N;Alternate names: kinase-related transforming protein pim-1
C;Species: Rattus norvegicus (Norway rat)
A;Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Accession: S26298
R;Wingett, D.; Reeves, R.; Magnuson, N.S.
A;Title: Characterization of the testes-specific pim-1 transcript in rat.
A;Reference number: S26298; MUID:92319652; PMID:1620615
A;Nucleic Acids Res. 20, 3183-3189, 1992
A;Molecule type: mRNA
A;Residues: 1-313 <WIN>
A;Cross-references: UNIPROT:P26794; UNIPARC:UPI0000131AD6; EMBL:X63675; NID:g56902; PIDN
A;Experimental source: testis
A;Note: testis-specific transcript is shorter and more stable than the somatic transcri
C;Function:
C;Superfamily: ATP; autophosphorylation; phosphoprotein; protein kinase homology <KIN>
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted

```
Query Match             98.0%;  Score 1636;  DB 1;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 9.2e-75;
Matches 304;  Conservative  6;  Mismatches  3;  Indels  0;  Gaps  0;

Qy      1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          ||||||||||||||||||| :|||||||||||||||||||||||||||||||||||:||
Db      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
```

RESULT 3
TVMSP1
protein kinase (EC 2.7.1.37) pim-1 - mouse
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24169
R;Selten, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.; v
A;Cell 46, 603-611, 1986
A;Title: The primary structure of the putative oncogene pim-1 shows extensive homology w
A;Reference number: A24169; MUID:86272109; PMID:3015420
A;Accession: A24169
A;Molecule type: DNA
A;Residues: 1-313 <SEL>
A;Cross-references: UNIPROT:P06803; UNIPARC:UPI0000294AF; GB:M13945; GB:M13946; NID:g920
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
C;Genetics:
A;Gene: pim-1
A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
C;Function:
C;Function: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Description:
A;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene; serine/threoni
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted

```
Query Match             94.7%;  Score 1582;  DB 1;  Length 313;
Best Local Similarity   93.9%;  Pred. No. 4.4e-72;
Matches 294;  Conservative 10;  Mismatches  9;  Indels  0;  Gaps  0;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
Db      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||| ||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIVKGQVFFRQRVSSECQHLIRWCLSRPSFEEIRNHPWMQGDLLPQETA 300
          ||||||| :|||||||||||||||||||||:||| : |  ||||| |||| 
Db    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPSFEEIRNHPWMQDVLLPQETA 300

Qy    301 EIHLHSLSPGPSK 313
          |||||||||||||
Db    301 EIHLHSLSPGPSK 313
```

RESULT 4
S55333
protein kinase pim-2 (EC 2.7.1.-) - mouse

C;Species: Mus musculus (house mouse)
C;Date: 10-Oct-1995 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S55333; A43093
R;van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; van der Gulden, H.; Alle...
EMBO J. 14, 2536-2544, 1995
A;Title: Proviral tagging in E-mu-myc transgenic mice lacking the Pim-1 proto-oncogene...
A;Reference number: S55333
A;Accession: S55333
A;Molecule type: mRNA
A;Residues: 1-370 <VAN>
A;Cross-references: UNIPROT:Q62070; UNIPARC:UPI000000028629; GB:L41495; NID:g9765065; PIDN:
A;Note: 40K form
A;Note: 37K form
A;Accession: B43093
A;Molecule type: mRNA
A;Residues: 'M',27-370 <VA2>
A;Cross-references: UNIPARC:UPI00000278BE; GB:L41495; NID:g9765065; PIDN:AAA98923.1; PID:
A;Accession: B43093
A;Molecule type: mRNA
A;Residues: 'M',61-370 <VA3>
A;Cross-references: UNIPARC:UPI00000278BF; GB:L41495; NID:g9765065; PIDN:AAA98924.1; PID:
A;Note: 34K form
C;Genetics:
C;Comment: Pim-2 autophosphorylates at unknown sites.
A;Genetics:
A;Gene: Pim-2
A;Map position: X
A;Start codon: CTG
A;Note: locus between A-raf and Act-7, near Kv4.1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin...
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphora...
F;89-345/Domain: protein kinase homology <KIN>
F;97-105/Region: protein kinase ATP-binding motif
F;120/Active site: Lys #status predicted

Query Match   52.8%; Score 881.5; DB 1; Length 370;
Best Local Similarity   56.6%;
Matches 171; Conservative 41; Mismatches 85; Indels 5; Gaps 2;

```
Qy    12 LRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGSGFGSVYSGIRVSDNLPVAIKHVEK  71
            ||||||| ::::| | | | ||  |||||||||||  ||||||:||:||  ::|||||::
Db    65 LQGHPSPVTPQPPGGKDRAAFEAEYRLGPLLGKGGFGTVFRAGHRVTDRRQVAIKVISR  124

Qy    72 DRISDWGELPNGTRVPMEVVLLKKV---SSGFSGVIRLLDWFERRDSFVLILERPEPVQDL 129
            :|:| |:||||||||||:| :|| :|:  ||||||||||:|||| :| ||||| :|:||
Db   125 NRVLGWSTVSDSVTCPLEVALLWKVGEGGNGHPGVIRLLDWFETPEGFMLVLERMPAQDL 184

Qy   130 FDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGS 189
            ||:||| | | | ||||| ||: | |:||| ||| |||||||||:|||||:|||||||||
Db   185 FDYITEKGPLGESCSRSFFTQVVAAVQHCHARGVVHRDIKDENLILDLCRGSIKLIDFGS 244

Qy   190 GALLKDTVYTDFDPGTRVSYSPPEWIRYHYRGHRSAAVWSLGILLYDMVCGDIPFEHDEII 249
            |||| | ::||||||||| | |||| ::|:|| :: | |||||||:|||||||||||||||
Db   245 GALLHDEPYTDFDPGTRVVSPPEWISRHQYHALPATVWSLGVLLYDMVCGDIPPERDQEIL 304

Qy   250 RGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETAEIHLHSLSP 309
            . | :||:::||: | ||| |||  |  |||||||::|||||  ||::::::  :: ||||
Db   305 EAELHFPAHVSPDCCALIRRCLAPKPCSRPSLEEILLDPWMQS---PAEEKPINSSKGSP 361

Qy   310 GP 311
Db   362 TP 363
```

RESULT 5
T22255
hypothetical protein F45H7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T22255
R;Percy, C.
submitted to the EMBL Data Library, June 1994

A;Reference number: Z19538
A;Accession: T22255
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:Q20443; UNIPARC:UPI00001755A4; EMBL:Z34800; PIDN:CAA84323.
A;Experimental source: clone F45H7
C;Superfamily: protein kinase homology

Query Match   36.9%; Score 617; DB 2; Length 363;
Best Local Similarity   45.3%;
Matches 120; Conservative 49; Mismatches 90; Indels 6; Gaps 3;

```
Qy    35 ESQYQVGPLLGSGSGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLK  94
          ::: ||||||| |||||:||  |:||: || |:||: |::  .| | |: :|||||:| |
Db    28 KKNYLKAELGRGGFGVVTRAVRICDNALVAVKFIERSNVKEWARI-NGEQVPMEICMLA  86

Qy    95 KVSSGFSGVIRLLDWFERRDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEA 154
          | ||  :|||||||||| ::| |:||||| |  |:||:| ||::||  ||||| :||  |
Db    87 KCSK-VRGVIRLLDWMYSIPEGFLIVWERPYPCIDMFDIKLIDFGQGKISEDMARFLRQIAVT 145

Qy   155 VRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDPGTRVSYSPPEWIR 214
          | .|.: ||||||:|||||:|||  | :||||||::  | | :|:|| |||| | |||| |
Db   146 VHECVQNRVLHRDLKDENIVIDLVTGSTKLIDFGAATVLRRSQYSDFQGTRLYCPPEWFL 205

Qy   215 YHYRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI----IRGQVFFRQRVSSECQHLIRWC 270
           | :||| :|||||||:|||:  ||| || :::||    | | | | |||||  | || ||
Db   206 HSLYLGREAAVWSLGVLLYNSLNGRLPFRNEKDICTAHLLGPLPFFVPVSAEVKDLISKC 265

Qy   271 LALRPSDRPTFEEIQNHPWMQDVLL 295
          | :   :| : | | ||||:: ::|
Db   266 LTFDPFQRCSLEAILNHPWVKQQTL 290
```

RESULT 6
T15435
hypothetical protein C06E8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15435
R;Favello, A.
submitted to the EMBL Data Library, February 1994
A;Description: The sequence of C. elegans cosmid C06E8.
A;Reference number: Z18350
A;Accession: T15435
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-409 <FAV>
A;Cross-references: UNIPARC:UPI000001B744; EMBL:U00034; NID:g458983; PID:g458986; PIDN
A;Experimental source: strain Bristol N2
A;Genetics:
A;Gene: CESP:C06E8.3
A;Introns: 24/1; 76/3; 107/2; 145/3; 199/1; 307/1; 375/1

Query Match   29.1%; Score 486; DB 2; Length 409;
Best Local Similarity   35.8%;
Matches 105; Conservative 55; Mismatches 125; Indels 8; Gaps 5;

```
Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGSGFGSVYSG-IRVS 59
           |:  |.: |  | ||| ||||||:| |      |||:|:||||| |||| |  |  |:||
Db     1 MIRKLQDLAVCCSYQVDFLHEKK----HSVKEFKRKYEVLDEIGRGGFGGGIVEATRQD 56

Qy    60 DNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERRDSFVLI 119
           .: |||:|:::: | ||   :  |   |:||: : :|  |  ||| | |||||||:|::
Db    57 GQQPVAVKFVQHKHVRSW-TMTCRQLIPSEVCHL-ETCEDIPGVIKILDWFANSKGFLIV 114

Qy   120 LERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHN-CGVLHRDIKDENILIDLN 178
           :|||   ||||| :: :| |: :| ||  |||: | :: : | || ||||||||||:::|
Db   115 MERPANCMDLFDMVSVHGPLNEDMGKFIFKQVITTVFNMYSKHGLLHRDIKDENLIVNMN 174
```

```
Qy    179 RGELKLIDFPGFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG 238
          |||| | |||| |  ||||||||||||||||||||||||||||||||||||||||||||
Db    175 TGEVKLVDFGATAYAEKATKKEFQGTRSYCPPEWFRDQLYLPLEATSWSLGVLLFILLTG 234

Qy    239 DIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQ 291
          ||| ||  ||    | | |  :::
Db    235 KLPFRNEIQICLGNVKFPPDLSKEVCQLVKSCLTTSTSARASLAQIAAHPWME 287
```

RESULT 7
I49072
protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I49072
R;Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A;Title: Identification of novel protein kinases expressed in the myocardium of the deve
A;Reference: I49071; MUID:95200798; PMID:7893599
A;Accession: I49072
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-481 <RES>
A;Cross-references: UNIPARC:UPI000017A422; EMBL:U11494; NID:g595420; PIDN:AAA67926.1; PI
C;Keywords: ATP
F;71-324/Domain: protein kinase homology <KIN>
F;79-87/Region: protein kinase ATP-binding motif

Query Match   23.1%; Score 386; DB 2; Length 481;
Best Local Similarity   33.9%; Pred. No. 1.3e-12;
Matches   99; Conservative   53; Mismatches 120; Indels   20; Gaps   10;

Qy   18 NDLHATKLAPGKEKPLE-SQYQVGPLLGSGGFGSV-YSGIRVSDNLPVAIKHVEKDRIS 75
         : | :| ||| | | || ||::|::|| | :: | :::||| || :|
Db   52 SEFRAVPSGTGRSQKPLRVGFYDVERTLGKGNFAVVKLRGHRVT-KTQVAIKIIDKTRL- 109

Qy   76 DWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITE 135
         : :: :: | ||| : :   : :| : :| :| : ::   : : ||:
Db   110 --DSSNLEKIYREVQLMKLLN-HPNIIKLYQVMETKDMLYIVTEFAKN-GEMFDYLTS 163

Qy   136 RGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLK- 194
         :| :: ||:|||:: :||::||: :|||||:||:|:| :| || |||| | |
Db   164 NGHLSENEARQKFWQILSAVEYCHNHHIVHRDLKTENLLLDSNM-DIKLADFGRGNFVKP 222

Qy   195 DTVYTDFDGTRVYSPPEWIRYRYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEI 248
         : : | ||:||||: | ::| |:: |||| |:|:||| :|| | |
Db   223 GEPLSTCVGSPPYVAAPEVFEGKEYEGPQLDVWSLGVVLVLVCGSLPFDGPNLPTLRQRV 282

Qy   249 IRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQ--DVLLPQE 298
         : | | | ::: ||| |:: ||:| | :: ||||:   :|| :
Db   283 LEGRFRIPFFMSQDCETLIRRMLVVDPAKRITIAQIRQHRWMQADPTLLQQD 334
```

RESULT 8
T13741
hypothetical protein 22E5.8 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13741
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: 217668
A;Accession: T13741
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1398 <MIR>
A;Cross-references: UNIPROT:O77268; UNIPARC:UPI000008020A3; EMBL:AL031765; NID:e1371523;
C;Genetics:
A;Cross-references: FlyBase:FBgn0000667
A;Residues: 1-1398 <MIR>
A;Introns: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3
A;Note: EG:22E5.8

Query Match   22.8%; Score 380; DB 2; Length 1398;
Best Local Similarity   33.3%; Pred. No. 6.2e-12;
Matches   92; Conservative   57; Mismatches 109; Indels   18; Gaps   9;

Qy   29 KEKEPLE-SQYQVGPLLGSGGFGSV-YSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRV 86
         | ||| || :||:| ||||| | :: | :::|:|||||:: :
Db   131 KLKEPMRVGFYDIERTIGKGNFAVVKLARHRITKN-EVAIKIIDKSQL----DQTNLQKV 185

Qy   87 PMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARS 146
         ::||: :::   : :| : :::| : : : | : :   :| : | : :: |:
Db   186 YREVEIMKRLK--HPHIIKLYQVMETKRNMIYIVSEYASQ-GEIFDYIAKYGRMSESAARF 242

Qy   147 FFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFG-SGALLKDTVYTDFDGTR 205
         :||:: :||::||: |:|||:|:|||:|:|:| :||:|||| :   :   : |
Db   243 KFWQIISAVEYCHKKGIVHRDLKAENLLLDLNM-NIKIADFGFSNHFKPGELLATWCCSP 301

Qy   206 VYSPPEWIRYRYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEIIRGQVFFRQRV 259
         :| ||||: | ::| |:: ||||: |:||| :|| | | : | | ||
Db   302 PYAAPEVFEGKQYTGPEIDIWSLGVVLYLVCGALPFDGSTLQSLRDRVLSGRFRIPFFM 361

Qy   260 SSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLL 295
         ||| :|||: |::: |: | | :: ||||| :||
Db   362 SSECEHLIRRMLVLEPTRRYTIDQIKRHRWMCPELL 397
```

RESULT 9
S66730
hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2034
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Oct-2004
C;Accession: S66730
R;Ansorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wiemann, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66723
A;Accession: S66730
A;Molecule type: DNA
A;Residues: 1-1101 <ANS>
A;Cross-references: UNIPROT:Q08217; UNIPARC:UPI000012DF35; EMBL:Z74788; NID:g1419846; PI
A;Experimental source: strain S288C
C;Genetics:
A;Cross-references: SGD:S0005405
A;Map position: 15L
C;Keywords: ATP
F;839-1099/Domain: protein kinase homology <KIN>
F;847-855/Region: protein kinase ATP-binding motif

Query Match     22.5%;  Score 376;  DB 2;  Length 1101;
Best Local Similarity     32.6%;  Pred. No. 8e-12;
Matches   87;  Conservative   59;  Mismatches 105;  Indels   16;  Gaps    6;

Qy    36 SQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLL 93
         |: :|  | |:|  | | : : : ::  :|:|  : :   : :|   | :  :  ||:
Db   839 SDFTILQVWGEGAYGKVNLCIHNREHYIVVIKMIFKERLLVDTWVRDRKLGTIPSEIQM 898

Qy    94 KKVS-SGFSGVIRLLDWFERPDSFVLILERPEPVQ------DLFDFITERGALQEELARS 146
         :    :  : :: ::|:|| ||: : |    :        :|||:|:| || :: :| :
Db   899 ATLNKNSQENILKLLDFFEDDDYYI------ETPVHGETGSIDLFDVIEFKKDMYEHEAKL 954

Qy   147 FFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRV 206
         :||:::  ::|:| :|:|||:|:|||:||  :|  |:|||||| |  :   |     |:
Db   955 VFKQVVASIKHLHDQGIVHRDIKDENIVD-SHGFVKLIDFGSAAYIKSGPFDVFVGTMD 1013

Qy   207 YSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFF--RQRVSSECQ 264
         |: ||:: |  ::|:  ::|:||:||: :: :::| :: ||      :   ::: |||
Db  1014 YAAPEVLGSSSYKGKPQDIWALGVLLYTIIYKSENPYYNIDEILEGELRLRFDKSEHVSECI 1073

Qy   265 HLIRWCLALRPSDRPTFEEIQNHPWMQ 291
         :|:: :|::::| ||| ||:  ||:|
Db  1074 SLIKRILTREVDKRPTIDEIYEDKWLK 1100
```

RESULT 10
S33653

Db   probable serine/threonine protein kinase (EC 2.7.1.-) - Yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 02-Aug-1994 #text_change 05-Oct-2004
R;Ouellette, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; D
C;Accession: S33653; S33717; S36732; JH0486
A;Reference number: S33653
A;Molecule type: DNA
A;Residues: 1-1358 <CLA>
A;Cross-references: UNIPROT:P31374; UNIPARC:UPI00000017A449; EMBL:L05146
R;Ouellette, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; D
submitted to the EMBL Data Library, January 1993
A;Description: Sequencing of Chromosome I from Saccharomyces cerevisiae enc
Yeast 9, 543-549, 1993
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac
A;Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae enc
R;Gumpel, N.J.
submitted to the EMBL Data Library
A;Accession: S33717
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Reference number: S33653; MUID:93311122; PMID:8322517
A;Residues: 1-1358
A;Cross-references: UNIPROT:UPI000005EA6; EMBL:L05146; NID:g171851; PIDN:AAC04940.1; PI
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
Yeast 8, 133-145, 1992
A;Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcriptiona
A;Reference number: S36732
A;Accession: S36732; MUID:92221690; PMID:1561836
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-862 <CL2>
A;Cross-references: UNIPARC:UPI00000017A44A; EMBL:S93805
R;Sidhu, R.S.; Mathews, S.; Bollon, A.P.
Gene 107, 111-118, 1991
A;Title: Selection of secretory protein-encoding genes by fusion with PHO5 in Saccharomy
A;Reference number: JH0483; MUID:92077420; PMID:1743509
A;Accession: JH0486
A;Molecule type: DNA
A;Residues: 1-72, 'E', 74-154 <SID>
A;Cross-references: SGD:S0000015; MIPS:YAL017w
A;Genetics:
C;Gene: SGD:FUN31; SSP138
A;Cross-references: UNIPARC:UPI00000017A44B
A;Map position: 1L
C;Keywords: ATP; glycoprotein; phosphotransferase; serine/threonine-specific protein kin
F;1096-1356/Domain: protein kinase homology <KIN>
F;1104-1112/Region: protein kinase ATP-binding motif
F;8,128/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1233/Active site: Asp #status predicted

Query Match   22.0%; Score 367; DB 2; Length 1358;
Best Local Similarity   33.7%; Pred. No. 2.7e-11;
Matches   87; Conservative   5; Mismatches 102; Indels 16; Gaps   6;

Qy   44 LGSGGFGSVYSGIRVSDNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLLKKVS-SGF 100
              :||::||||||||:|||||||||||||||: ||:|||||||||||||||| ::|
Db   1104 MGEGAYGKVNLCIHKKRYIVIVKMIFKERILVDTWTWRDRKLGTIPSEIQIMATLNKKPH 1163

Qy   101 SGVIRLLDWFERPDSFVLILERPEPVQ-------DLFDFITERGALQEELARSFFWQVLEA 154
              ||:|||||||:||||||:||||:||| :|:|:|||||||:|||||||||:|:
Db   1164 ENILRLLDFPEDDDYYI------ETPVHGETGCIDLFDLIEFKINMTEFEAKLIFKQVVAG 1219

Qy   155 VRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVVSPPEWIR 214
              |::|||:|||||||||||||:|||||||||||||||||:|||||||||||||||||||
Db   1220 IKHLHDQIVHRDIKDENVIVD-SKGFVKIIDFGSAAVKSGPFDVFVGTIDYAAPEVLG 1278

Qy   215 YHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFR--QRVSSECQHLIRWCLA 272
              ||:|||||||||||||||||||:|||||||||:|:|||||| ||:||||||||||:
Db   1279 GNPYEYGQPQDIWAIGILLYTVVFKENPFYNIDEILEGDLKFNNAEEVSEDCIELIKSTIN 1338

Qy   273 LRPSDRPTFEEIQNHPWM 290
              :|:::||||:|||||:
Db   RCVPKRPTIDDINNDKWL 1356

RESULT 11
T10449

Db   probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N;Alternate names: SNF1-related protein kinase
C;Species: Cucumis sativus (cucumber)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-Oct-2004
C;Accession: T10449
R;Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z17020
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-504 <GUM>
A;Cross-references: UNIPROT:P93113; UNIPARC:UPI00000A4B92; EMBL:Y10036
A;Experimental source: cv. Masterpiece; cotyledon
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>

Query Match   21.9%; Score 366; DB 2; Length 504;
Best Local Similarity   34.4%; Pred. No. 1.3e-11;
Matches   90; Conservative   51; Mismatches 105; Indels 16; Gaps   8;

Qy   38 YQVGPLLGSCGFGSVYYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
              :|||:|| :|||:|||||||||||||||||||||||:|::|||||||||||||||||||
Db   8 YKLGKTLGIGSFGKVKIAEHALTGHKVAIKILNRRKIKN--LDMEEKVRREIKILRLFM 64

Qy   98 SGFGSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
              ||:| ||:||||||:||||:|||||:||:||||::|||||||:|||||||||:|:
Db   65 --HPHIIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 121

Qy   158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVVSPPEWIRYH 216
              ||:|||||||||||||:||||||||||||||||||:|||||||: |||||||||||||
Db   122 CHRNMVVHRDLKPENLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 180

Qy   217 RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----IRGQVF-FRQRVSSECQHLIRW 269
              |||||||||||||||||||:||||||||||: ||||| ||::|||||||||:
Db   181 LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELPS 239

Qy   270 CLALRPSDRPTFEEIQNHPWMMQ 291
              |||:|:::|||||||||||:|
Db   240 MLVVDPMKRITIPEIRQHPWFQ 261

RESULT 12
S52244

Db   p69Eg3 protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: S52244
R;Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A;Description: Eg3, selected by differential screening encodes a new Xenopus protein k
A;Reference number: S52243
A;Accession: S52244
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-651 <ROG>
A;Cross-references: UNIPROT:Q91821; UNIPARC:UPI00000017A463; EMBL:Z17205; NID:g609283; P
C;Keywords: ATP
F;11-265/Domain: protein kinase homology <KIN>
F;19-27/Region: protein kinase ATP-binding motif

Query Match   21.6%; Score 361; DB 2; Length 651;
Best Local Similarity   34.8%; Pred. No. 2.8e-11;
Matches   94; Conservative   51; Mismatches 103; Indels 22; Gaps   8;

```
Qy    32 EPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVV 91
         :|| ::|:||||| | ||:|| ||||||::|:||:::::|:|: :|||||||||||||
Db     7 EELLKYELHETVGTGGFAKVKLASHLITGEKVAIKIMDKESLGD--DLP---RVKTEID 61

Qy    92 LLKKVSSGGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEBLARSFFWQV 151
         ||| ::| :| ||||||||| |||||||||||||||||||||||||||||||||||||
Db    62 AMKNLS--HQHVCRLYHVIETPKKIFMVLEYC-PGGELFDYIIAKDRLTEEEARVFFRQI 118

Qy   152 LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-----GTRV 206
         ||||||| | ||||||||||||||||||||||||||||||||||| ||||     | |
Db   119 VSAVAYIHSQGYAHRDLKPENLLIDEDQ-NLKLIDFGLCAKPKGGL--DYHLMTCCGSPA 175

Qy   207 YSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEIIRGQVFFRQRVS 260
         :| : :|| ||||||||||||| ||| |   |:||| |     ||||||  ||| :
Db   176 YAAPELIQGKAYIGSEADIWSMGVLMYALMCGYLPFDDDNVMVLYKKIMRGKYEIPKWLS 235

Qy   261 SECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
         | |:|||||||||||||| |||| |:|||
Db   236 PGSVLLLSQMMQVDPKKRITVKHLLNHPWL 265
```

RESULT 13

JC7500

qik protein - chicken
N;Alternate names: Qin-induced kinase
C;Species: Gallus gallus (chicken)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7500
A;Molecule type: DNA
R;Xia, Y.; Zhang, Z.; Kruse, U.; Vogt, P.K.; Li, J.
Biochem. Biophys. Res. Commun. 276, 564-570, 2000
A;Title: The new serine-threonine kinase, Qik, is a target of the qin oncogene.
A;Reference number: JC7500
A;Contents: Embryo fibroblasts
A;Accession: JC7500
A;Molecule type: mRNA
A;Residues: 1-798 <XIA>
A;Cross-references: UNIPROT:Q91A88; UNIPARC:UPI000044792; GB:AF212232
C;Comment: This protein, a member of the AMPK/SNF1 family of serine/threonine kinases, f

```
Query Match             21.6%;  Score 361;  DB 2;  Length 798;
Best Local Similarity   32.7%;
Matches   88;  Conservative   50;  Mismatches 115;  Indels 16;  Gaps 7;

Qy    38 YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
         |:|| ||| | || :|:||:|: :::||||:||::||||||:: :||: :::::| :|
Db    26 YDIERTLGKGNFAVVKLARHRVRTKQVAIKIIDKTRL-----DPSNLEKIYREVQIMKLLN 81

Qy    98 SGGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEBLARSFFWQVLEAVRH 157
         ||  ||::|| | ||::   :||:|:  |:||| ||:|:|||:: |||::||:|:| |
Db    82 --HPHIIKLYQVMETKDMLYIVTEFAKN-GEMFDHLTSNGHLSSEARKFWQILSAVEY 138

Qy   158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD-TVYDFDGTRVYSPPEWIRYH 216
         | | |||||:|: ||:||||  || ||||||  ||   ||  || |||||| |||:|
Db   139 CHSHHIVRDLKTENLLLDANM-NIKLADFGFGNFYKSGGEPLSTWCGSPPYAAPEVFEGK 197

Qy   217 RYHGRSAAVWSLGILLLYDMVCGDIPFEHD------EEIIRGQVFFRQRVSSECQHLIRWC 270
          |||||| |||:|||: ||:| ||  ||       ||||||:||| :| |::||:||||
Db   198 EYEGPHLDIWSLGVVLVLVCGSLPFDGENLPTLRQRVLEGRFRIPYFMSEDCETLIRRM 257

Qy   271 LALRPSDRPTFEEIQNHPWMQ-DVLLPQE 298
         | |||||||||||:|||||||  |  | |
Db   258 LVVDPTKRITISQLKQHKWMQADPSLRQQ 286
```

RESULT 14

JC1446

serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana
N;Alternate names: protein kinase SNF1 homolog
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Oct-2004

C;Accession: JC1446; S58266; S66334
R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
A;Reference number: JC1446; MUID:93013041; PMID:1339373
A;Accession: JC1446
A;Molecule type: DNA
A;Residues: 1-512 <LEG>
A;Cross-references: UNIPROT:Q38997; UNIPARC:UPI000012DE43; GB:M93023; NID:g166599; PIDN:
R;Thuemmler, F.; Kircher, M.; Teuber, R.; Dittrich, P.
submitted to the EMBL Data Library, May 1995
A;Description: Differential accumulation of the transcripts of 22 novel protein kinase g
A;Reference number: S58266
A;Molecule type: DNA
A;Accession: S58266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 144-198 <THU>
A;Cross-references: UNIPARC:UPI00009DEE0; EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PI
R;Thuemmler, F.; Kircher, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes i
A;Reference number: S66314; MUID:96123233; PMID:8534852
A;Accession: S66334
A;Molecule type: DNA
A;Residues: 144-198 <TH2>
A;Cross-references: UNIPARC:UPI00009DEE0; EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PI
C;Genetics:
A;Gene: AKin10; AK21
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
A;Gene: AKin10; AK21
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted

```
Query Match             21.6%;  Score 360;  DB 1;  Length 512;
Best Local Similarity   33.6%;
Matches   90;  Conservative   51;  Mismatches 111;  Indels 16;  Gaps 8;

Qy    32 EPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVV 91
         | ||| ||:||:| |||| ||| | ||: |||||:|||:||:|||||||||||||||:||
Db    13 ESILPNYKLGRTLGIGSFGRVKIAEHALTGHKVAIKILNRRKIKN--MEMEBKVRREIK 69

Qy    92 LLKKVSSGGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEBLARSFFWQV 151
         || | :| :| | | |: | |   :|:|:||| | |||| ||:|:|:| |: |||:||||
Db    70 ILRLFM--HPHIIRLYEVIETPTDIYLVMEYVNS-GELFDYIVEKGRLQEDEARNFFQQI 126

Qy   152 LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-----GTRV 206
         |||||| |  |:|||||||||:||||  ||||||||| : | |  :::|:|     |||
Db   127 ISGVEYCHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAP 185

Qy   207 YSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFEHDEEI-----IRGQVP-FRQRVS 260
         |||| ::| |||||||| |||:|| |||:| | :|||||:     |||||| |||| |
Db   186 EVIGGKLYAGPEVDVWSCGVILALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSPGA 244

Qy   261 SSECQHLIRWCLALRPSDRPTFEEIQNHPWMQ 291
         :|| | |||||||||||| |:|||:|||||
Db   245 RDLIPRMLVVDPMKRVTIPEIRQHPWFQ 272
```

RESULT 15

A56009

serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 05-Oct-2004
C;Accession: A56009
R;Muranaka, T.; Banno, H.; Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A;Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces cer

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tase of Saccharomyces cerevisiae.
A;Reference number: A56009; MUID:9421769B; PMID:8164654
A;Accession: A56009
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-511 <MUR>
A;Cross-references: UNIPROT:Q40544; UNIPARC:UPI00000AAD0C; GB:D26602; NID:g496384; PIDN:
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match         21.5%;   Score 359;   DB 1;   Length 511;
Best Local Similarity   31.7%;   Pred. No. 2.9e-11;
Matches   86;   Conservative   54;   Mismatches 117;   Indels  14;   Gaps   6;

Qy     28 GKEKEPLESQYQVGPLLGGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP     87
              | :||||         |  || |  |  ::|   :  :
Db      9 GSSVESFLRNYKLGKTLGIGSFGKVKIAEHTLTGHKVAVKILNRRKIKN---MEMEEKVR     65

Qy     88 MEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSF    147
            | :| ||    |  || :|  ::| |   |:  :| :  ::|  : : || ::
Db     66 REIKILRLFM--HPHIIRLYEVETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARKF    122

Qy    148 FWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRV    206
            :| :| |  |  | | | |||||:||   :|||||||:|||     :  : | ||  |  ||
Db    123 FQQIISGVEYCHRNMVVHRDLKPENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPN    181

Qy    207 YSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD--------EEIIRGQVFFRQRVS    260
             :  | ||    |      |  || | |   | |        :| :|||  |  |
Db    182 YAAPEVISGKLYAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFKKIKGGMISLPSHLS    241

Qy    261 SECQHLIRWCLALRPSDRPTFEEIQNHPWMQ    291
            :  |  ||  :  |  |  :  |  |  | ||
Db    242 AGARDLIPRMLIVDPMKRMTIPEIRMHPWFQ    272
```

Search completed:May 4, 2006, 05:25:50
Job time : 22.3333 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: May 4, 2006, 05:12:40 ; Search time 122 seconds
(without alignments)
1810.085 Million cell updates/sec

Title: US-10-705-757-2
Perfect score: 1670
Sequence: 1 MLLSKINSLAHLRAAPCNDL.........LLPQETAEIHLHSLSPGPSK 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1670	100.0	313	1	PIM1_HUMAN	P11309 homo sapien
2	1670	100.0	313	2	Q5TH7_HUMAN	Q5TH7 homo sapien
3	1659	99.3	313	1	PIM1_FELCA	Q95I0 felis silve
4	1656	99.2	313	1	PIM1_BOVIN	Q9n0p9 bos taurus
5	1636	98.0	313	1	PIM1_RAT	P26794 rattus norv
6	1587	95.0	313	2	Q8CFN8_MOUSE	Q8cfn8 mus musculu
7	1582	94.7	313	1	PIM1_MOUSE	P06803 mus musculu
8	1140	68.3	313	1	PIM3_COTJA	Q9pu85 coturnix co
9	1133	67.8	326	1	PIM3_HUMAN	Q86V86 homo sapien
10	1129.5	67.6	326	1	PIM3_MOUSE	P58750 mus musculu
11	1128.5	67.6	326	1	PIM3_RAT	O70444 rattus norv
12	1128.5	67.6	380	2	Q4V8M2_RAT	Q4v8m2 rattus norv
13	1116	66.8	325	2	Q811X8_MOUSE	Q811x8 mus musculu
14	1105	66.2	323	1	PIM3_XENLA	Q91822 xenopus lae
15	1101	65.9	318	2	Q66III_XENTR	Q66iii xenopus tro
16	1092	65.4	337	2	Q5U489_XENLA	Q5u489 xenopus lae
17	1065	63.8	316	2	Q4STF0_TETNG	Q4stf0 tetraodon n
18	881.5	52.8	311	2	Q8R2P0_MOUSE	Q8r2p0 mus musculu
19	881.5	52.8	370	1	PIM2_MOUSE	Q62070 mus musculu
20	869.5	52.1	311	1	PIM2_HUMAN	Q9p1w9 homo sapien
21	854	51.1	310	2	Q7ZVJ5_BRARE	Q7zvj5 brachydanio
22	851	51.0	310	2	Q8JFW9_BRARE	Q8jfw9 brachydanio
23	846	50.7	310	1	PIM1_BRARE	Q6yh25 brachydanio
24	844	50.5	310	2	Q6D152_BRARE	Q6d152 brachydanio
25	799.5	47.9	288	2	Q4TDC2_TETNG	Q4tdc2 tetraodon n
26	716.5	42.9	221	2	Q8RIZ0_MOUSE	Q8riz0 mus musculu
27	626	37.5	500	2	Q61B7_CAEBR	Q61jb7 caenorhabdi
28	617	36.9	441	2	Q20443_CAEEL	Q20443 caenorhabdi
29	497	29.8	566	2	Q61228_CAEBR	Q61228 caenorhabdi
30	486	29.1	378	2	Q8T3F1_CAEEL	Q8t3f1 caenorhabdi
31	486	29.1	566	2	Q17737_CAEEL	Q17737 caenorhabdi
32	440	26.3	270	2	Q5SPE4_BRARE	Q5spe4 brachydanio
33	423	25.3	465	2	Q5SPF6_BRARE	Q5spf6 brachydanio
34	421.5	25.2	134	2	Q6P2J9_HUMAN	Q6p2j9 homo sapien
35	421	25.2	416	2	Q4RFY6_TETNG	Q4rfy6 tetraodon n
36	412	24.7	281	2	Q5SV44_BRARE	Q5sv44 brachydanio
37	403	24.1	125	2	Q6Q2K5_CANFA	canis famil
38	394.5	23.6	268	2	Q5PP9_BRARE	Q5pp9 brachydanio
39	391.5	23.4	578	2	Q5RH93_BRARE	Q5rh93 brachydanio
40	389.5	23.3	1383	1	PASK_MOUSE	mus musculu
41	388	23.2	463	2	Q8CEE6_MOUSE	Q8cee6 mus musculu
42	388	23.2	465	2	Q5RG24_BRARE	Q5rg24 brachydanio
43	388	23.2	465	2	Q5RG26_BRARE	Q5rg26 brachydanio
44	388	23.2	1385	2	Q5TYR9_BRARE	Q5tyr9 brachydanio
45	387	23.2	1107	2	Q6C310_YARLI	Q6c310 yarrowia li

ALIGNMENTS

RESULT 1
PIM1_HUMAN

PIM1_HUMAN STANDARD; PRT; 313 AA.

ID PIM1_HUMAN
AC P11309; Q96RG3;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN Name=PIM1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
RA Zakut-Houri R., Hazum S., Givol D., Telerman A.;
RT "The cDNA sequence and gene analysis of the human pim oncogene.";
RL Gene 54:105-111(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88217305; PubMed=3329709;
RA Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
RA Berns A.;
RT "Comparison of the human and mouse PIM1 cDNAs: nucleotide sequence
RT and immunological identification of the in vitro synthesized PIM1
RT protein.";
RL Oncogene Res. 1:103-112(1987).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88115604; PubMed=3429489;
RA Meeker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
RT "Cloning and characterization of the human PIM-1 gene: a putative
RT oncogene related to the protein kinases.";
RL J. Cell. Biochem. 35:105-112(1987).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RL   "Generation and initial analysis of more than 15,000 full-length human
RL   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   NUCLEOTIDE SEQUENCE OF 1-202.
RX   MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085588;
RA   Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
RA   Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
RT   "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
RT   cell lymphomas.";
RL   Nature 412:341-346(2001).
RN   [7]
RP   CHARACTERIZATION.
RX   MEDLINE=88246418; PubMed=2837645;
RA   Telerman A., Amson R., Zakut-Houri R., Givol D.;
RT   "Identification of the human pim-1 gene product as a 33-kilodalton
RT   cytoplasmic protein with tyrosine kinase activity.";
RL   Mol. Cell. Biol. 8:1498-1503(1988).
RN   [8]
RP   FUNCTION.
RX   MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
RA   Koike N., Maita H., Taira T., Ariga H., Iguchi-Ariga S.M.M.;
RT   "Identification of heterochromatin protein 1 (HP1) as a
RT   phosphorylation target on the transcriptional repression function of HP1.";
RL   FEBS Lett. 467:17-21(2000).
RN   [9]
CC   -!- SUBCELLULAR LOCATION.

CC   -!- FUNCTION: Thought to play a role in signal transduction in blood
CC   cells. May affect the structure or silencing of chromatin by
CC   phosphorylating HP1 gamma/CBX3.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC   -!- TISSUE SPECIFICITY: Expressed primarily in cells of the
CC   hematopoietic and germ line lineages.
CC   -!- PTM: Autophosphorylated on tyrosine residues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC   WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PIM1ID261.html".

DR   PDB; 1YHS; X-ray; A=33-305.
DR   PDB; 1Y13; X-ray; A=33-305.
DR   PDB; 1Y14; X-ray; A=33-305.
DR   PDB; 2BIK; X-ray; B=1-313.
DR   PDB; 2BIL; X-ray; B=1-313.
DR   PDB; 2BZH; X-ray; B=1-313.
DR   Ensembl; ENSG00000137193; Homo sapiens.
DR   HGNC; HGNC:8986; PIM1.
DR   H-InvDB; HIX0005835; -.
DR   MIM; 164960; -.
DR   GO; GO:0005737; C:cytoplasm; TAS.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR   GO; GO:0007275; P:development; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   3D-structure; ATP-binding; Kinase; Nuclear protein;
KW   Nucleotide-binding; Phosphorylation; Proto-oncogene;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   38   290   Protein kinase.
FT   NP_BIND   44   52   ATP (By similarity).
FT   ACT_SITE   167   167   Proton acceptor (By similarity).
FT   BINDING   67   67   ATP (By similarity).
FT   CONFLICT   15   15   AP -> RA (in Ref. 2).
SQ   SEQUENCE   313 AA; 35686 MW; 35BA76D3668B69A3 CRC64;

Query Match   100.0%; Score 1670; DB 1; Length 313;
Best Local Similarity   100.0%; Pred. No. 7.2e-115;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
              |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 2
Q5TH7_HUMAN
Q5TH7_HUMAN PRELIMINARY;   PRT;   313 AA.
ID   Q5TH7_HUMAN
AC   Q5TH7;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Pim-1 oncogene (Proviral integration site 1).
GN   Name=PIM1; ORFNames=RP3-355M6.1-003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;

DR   EMBL; M27903; AAA60090.1; -; Genomic_DNA.
DR   EMBL; M16750; AAA60089.1; -; mRNA.
DR   EMBL; M54915; AAA36447.1; -; mRNA.
DR   EMBL; M24779; AAA81553.1; -; mRNA.
DR   EMBL; BC020224; AAH20224.1; -; mRNA.
DR   EMBL; AF386792; AAK70871.1; -; Genomic_DNA.
DR   PIR; JU0327; TVHUP1.
DR   PDB; 1XQZ; X-ray; A=14-313.
DR   PDB; 1XR1; X-ray; A=14-313.
DR   PDB; 1XWS; X-ray; A=1-313.

```
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Laird G.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AL353579; CAI20316.1; -; Genomic_DNA.
DR   SMR; Q5T7H7; 32-308.
DR   Ensembl; ENSG00000137193; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   313 AA;  35686 MW;  35BA76D3668E69A3 CRC64;

Query Match             100.0%;  Score 1670;  DB 2;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 7.2e-115;
Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313
```

```
RESULT 3
PIM1_FELCA
ID   PIM1_FELCA     STANDARD;      PRT;   313 AA.
AC   Q95LJ0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fujino Y., Satoh H., Hisasue M., Masuda K., Ohno K., Tsujimoto H.;
RT   "The cDNA sequence of the feline pim-1 oncogene.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; AB073748; BAB71752.1; -; mRNA.
DR   SMR; Q95LJ0; 32-308.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN       38    290       Protein kinase.
FT   NP_BIND      44     52       ATP (By similarity).
FT   ACT_SITE    167    167       Proton acceptor (By similarity).
FT   BINDING      67     67       ATP (By similarity).
SQ   SEQUENCE   313 AA;  35686 MW;  C0BE268D638B6967 CRC64;

Query Match              99.3%;  Score 1659;  DB 1;  Length 313;
Best Local Similarity    99.0%;  Pred. No. 4.6e-114;
Matches  310;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||:|
Db          1 MLLSKINSLAHLRTAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313
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RESULT 4
PIM1_BOVIN
ID   PIM1_BOVIN     STANDARD;      PRT;   313 AA.
AC   Q9N0P9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Left column

```
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21109090; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2;
RA   Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;
RT   "cDNA cloning, sequencing and characterization of bovine pim-1.";
RL   Vet. Immunol. Immunopathol. 78:177-195(2001).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
```

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DR   EMBL; AF259078; AAF67200.1; -; mRNA.
DR   HSSP; Q63450; 1A06.
DR   SMR; Q9N0P9; 32-308.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN        38    290       Protein kinase.
FT   NP_BIND       44     52       ATP (By similarity).
FT   ACT_SITE     167    167       Proton acceptor (By similarity).
FT   BINDING       67     67       ATP (By similarity).
SQ   SEQUENCE   313 AA;  35630 MW;  9EF40229A847AD47 CRC64;

Query Match             99.2%;  Score 1656;  DB 1;  Length 313;
Best Local Similarity   98.7%;
  Matches  309;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCSDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHDCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              |||||||:|||:||:|||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIVRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313

RESULT 5
PIM1_RAT
ID   PIM1_RAT      STANDARD;      PRT;   313 AA.
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Right column

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AC   P26794;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=Pim1; Synonyms=Pim-1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
     STRAIN=Sprague-Dawley; TISSUE=Testis;
     MEDLINE=92319652; PubMed=1620615;
RA   Wingett D., Reeves R., Magnuson N.S.;
RT   "Characterization of the testes-specific pim-1 transcript in rat.";
RL   Nucleic Acids Res. 20:3183-3189(1992).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
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DR   EMBL; X63675; CAA45214.1; -; mRNA.
DR   PIR; S26298; S26298.
DR   SMR; P26794; 32-308.
DR   Ensembl; ENSRNOG00000000529; Rattus norvegicus.
DR   RGD; 3330; Pim1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Kinase; Nuclear protein; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN        38    290       Protein kinase.
FT   NP_BIND       44     52       ATP (By similarity).
FT   ACT_SITE     167    167       Proton acceptor (By similarity).
FT   BINDING       67     67       ATP (By similarity).
SQ   SEQUENCE   313 AA;  35631 MW;  D5757DA9F1821BF9 CRC64;

Query Match             98.0%;  Score 1636;  DB 1;  Length 313;
Best Local Similarity   97.1%;
  Matches  304;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||:|
Db          1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHDCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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RESULT 6

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Qy  241 PFEHDEEIVKGQVFPRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||:|||||| |:|||||||||:||||:||||||||||| ::|||||| ||||   ||
Qy  301 EIHLHSLSPGPSK 313
        |||||||| ||||
Db  301 EIHLHSLSPSPSK 313
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ID   Q8CFN8_MOUSE PRELIMINARY;   PRT;   313 AA.
AC   Q8CFN8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Proviral integration site 1.
GN   Name=Pim1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX   MEDLINE=22382857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McKernan P.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
DR   EMBL; BC042285; AAH42285.1; -; mRNA.
DR   EMBL; BC053019; AAH53019.1; -; mRNA.
DR   EMBL; BC055316; AAH55316.1; -; mRNA.
DR   SMR; Q8CFN8; 32-308.
DR   Ensembl; ENSMUSG00000024014; Mus musculus.
DR   MGI; MGI:97584; Pim1.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase;
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   313 AA; 35451 MW; 1294F16A03B7C7D7 CRC64;

Query Match   95.0%; Score 1587; DB 2; Length 313;
Best Local Similarity   94.2%; Pred. No. 9.3e-109;
Matches 295; Conservative   10; Mismatches   8; Indels   0; Gaps   0;

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Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
        ||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||:|||||||||||||||:|
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILLDLNRG 180
        |||||||||||||||||||||:|||:||||||||||||||||||||||||||||||||:.||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILLDLSRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        ||||||||:|||||:|||.||||||||||:||:||||||.::|||||||:||| |||:
Db  241 PFEHDEEIKGQVFPRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPSPSK 313
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RESULT 7

ID   PIM1_MOUSE   STANDARD;   PRT;   313 AA.
AC   P06803;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=Pim1; Synonyms=Pim-1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
RA   Selten G., Cuypers H.T., Boelens W., Robanus-Maandag E., Verbeek J.,
RA   Domen J., van Beveren C., Berns A.;
RT   "The primary structure of the putative oncogene pim-1 shows extensive
RT   homology with protein kinases.";
RL   Cell 46:603-611(1986).
RN   [2]
RP   INTERACTION WITH RP9.
RX   MEDLINE=20389540; PubMed=10931201;
RA   Maita H., Harada Y., Nagakubo D., Kitaura H., Ikeda M., Tamai K.,
RA   Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
RT   "PAP-1, a novel target protein of phosphorylation by Pim-1 kinase.";
RL   Eur. J. Biochem. 267:5168-5178(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).

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Qy  241 PFEHDEEIVKGQVFPRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||:|||||:|||.||||||||||:||||||||||||||:|||||||:||| |||:
Db  241 PFEHDEEIKGQVFPRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGPSK 313
        |||||||| ||||
Db  301 EIHLHSLSPSPSK 313
```

CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- DISEASE: Frequently activated by provirus insertion in murine
CC   leukemia virus-induced T-cell lymphomas.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   ---
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---
DR   EMBL; M13945; AAA39930.1; -; Genomic_DNA.
DR   PIR; A24169; TVMSP1.
DR   HSSP; Q63450; 1AO6.
DR   SMR; P06803; 32-308.
DR   Ensembl; ENSMUSG00000024014; Mus musculus.
DR   MGI; MGI:97584; Pim1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN   38   290   Protein kinase.
FT   NP_BIND   44   52   ATP (By similarity).
FT   ACT_SITE   167   167   Proton acceptor (By similarity).
FT   BINDING   67   67   ATP (By similarity).
SQ   SEQUENCE   313 AA; 35537 MW; 79F4779E9DCBDC16 CRC64;

Query Match   Best Local Similarity   94.7%;
                        Score 1582; DB 1; Length 313;
Matches 294; Conservative   10; Mismatches   9; Indels   0; Gaps   0;
                        Pred. No. 2.2e-108;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVSD 60
           ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||| |
Db   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy   121 EREPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           ||||||||||||||||||||||:|||.|||||||||||||||||||||||||||||||.||
Db   121 EREPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECOHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
           |||||||:|.|||||||:||||||||:|||.|||||||.||||.|||.||.| ||||..:
Db   241 PFEHDEEIIKGQVFFRQTVSSECOHLIKWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS 300

Qy   301 EIHLHSLSPGPSK 313
           ||||||||||.||
Db   301 EIHLHSLSPGSSK 313

RESULT 8
PIM3_COTJA
ID   PIM3_COTJA   STANDARD;   PRT;   323 AA.
AC   Q9PUB5;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (qpim).
GN   Name=Pim3; Synonyms=PIM-3;
OS   Coturnix coturnix japonica (Japanese quail).

OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=93934;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20180111; PubMed=10713710; DOI=10.1038/sj.onc.1203355;
RA   Eichmann A., Yuan L., Breant C., Alitalo K., Koskinen P.J.;
RT   "Developmental expression of Pim kinases suggests functions also
RT   outside of the hematopoietic system.";
RL   Oncogene 19:1215-1224(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   ---
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---
DR   EMBL; AJ130845; CAB62386.1; -; mRNA.
DR   HSSP; Q63450; 1AO6.
DR   SMART; SM00220; S_TKc; 1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   InterPro; IPR002290; Ser_Thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   40   291   Protein kinase.
FT   NP_BIND   46   54   ATP (By similarity).
FT   ACT_SITE   168   168   Proton acceptor (By similarity).
FT   BINDING   69   69   ATP (By similarity).
SQ   SEQUENCE   323 AA; 36597 MW; E2A4FA20B6F6396C CRC64;

Query Match   Best Local Similarity   67.4%;
                        Score 1140; DB 1; Length 323;
Matches 209; Conservative   45; Mismatches   52; Indels   4; Gaps   3;
                        Pred. No. 8e-76;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAP--GKEKEPLESQYQVGPLLGSSGFGSVYSGIRV 58
           |||||..|||| .| | ||.| | | |||||| .::.|||.:||||.||:||:| :
Db   1 MLLSKFGSLAHICSPASMDHLPVKILPPVVKEKEPFDKVYQVGSVLGSSGGFGTVYAGSRI 60

Qy   59 SDNLPVAIKHVEKDRISDWGELPNGTRVVMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVL 118
           :|.|||.:||..:.|.|.||.: |. .: ||:|||||||||.|.||:.||||:|||:.|.:
Db   61 ADGLPVAVKHVVKERVTEWGTI-GGVVMPLEIVLLKKVSSGFRGVIKLLDWYERPDGFLI 119

Qy   119 ILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLN 178
           ::|||| |:|||||||.:||||:|.||.|.:|||||||||...||:.|||||||:|.||:
Db   120 VMERPELVKDLFDFITEKGALDEDTARGFPRQVLEAVRHCYGCGVVHRDIKDENLLVDLR 179

Qy   179 RGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG 238
           .||||||||||||||||||||||||||||||||||||||||||||:.||||:|||||||||
Db   180 TGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDMVCG 239

Qy   239 DIPFEHDEEIIRGQVFFRQRVSSECOHLIRWCLALRPSDRPTFEEIQNHPWM-QDVLLPQ 297
           ||||| ||||.|.. :||.|:| |||.|||||| ||||||||| | | ||.|| :.:
Db   240 DIPFEQDEEILRGRLYFRRRISPECOQLIKWCLSLRPSDRPTLEQIFDHQWMHKSEVVKS 299

Qy   298 ETAEIHLHSL 307
           :..::.| .
Db   300 EDCDIRLRTL 309

RESULT 9
PIM3_HUMAN
ID   PIM3_HUMAN   STANDARD;   PRT;   326 AA.

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AC   Q86V86; Q68BM2;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=PIM3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY.
RC   TISSUE=Liver;
RX   PubMed=15540201; DOI=10.1002/ijc.20719;
RA   Fujii C., Nakamoto Y., Lu P., Tsuneyama K., Popivanova B.K.,
RA   Kaneko S., Mukaida N.;
RT   "Aberrant expression of serine/threonine kinase Pim-3 in
RT   hepatocellular carcinoma development and its role in the proliferation
RT   of human hepatoma cell lines.";
RL   Int. J. Cancer 114:209-218(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   IDENTIFICATION FROM ESTS.
RX   MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;
RA   Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.;
RT   "Consistency checks for characterizing protein forms.";
RL   Comput. Biol. Chem. 27:29-35(2003).
-!- FUNCTION: May be involved in cell cycle progression and anti-
CC       apoptosis process. Implicated in proliferation of human hepatoma
CC       cell lines.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- TISSUE SPECIFICITY: Widely expressed. No expression in colon,
CC       thymus, and small intestine. Expressed in human hepatoma cell
CC       lines but not in normal liver tissues.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
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DR   EMBL; AB114795; BAD42438.1; -; mRNA.
DR   EMBL; BC052239; -; NOT_ANNOTATED_CDS; mRNA.
DR   Ensembl; ENSG00000198355; Homo sapiens.
DR   HGNC; HGNC:19310; PIM3.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pKin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       40    293       Protein kinase.
FT   NP_BIND      46     54       ATP (By similarity).
FT   ACT_SITE    170    170       Proton acceptor (By similarity).
FT   BINDING      69     69       ATP (By similarity).
SQ   SEQUENCE   326 AA;  35863 MW;  41FDF9DD2467A162 CRC64;
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Query Match             67.8%;   Score 1133;  DB 1;  Length 326;
Best Local Similarity   69.3%;
Matches  219;  Conservative  35;  Mismatches  52;  Indels  10;  Gaps  7;

Qy     1 MLLSKINSLAHLRAAP--CNDLHATKLIAPGK-EKEPLESQYQVGPLLGSSGFGSVYSGIR 57
           |||||||||||:         |: :|||  |: ||:|||||||||| |:|::||| ||:|
Db     1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYAGSR 59

Qy    58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSVGVIRLLLDWFERPDS 115
           :|: ||||:||| |:|:  ||.|  ||.||:||||:|||  :.| . |||||||||||| |
Db    60 IADGLPVAVKHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy   116 FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
           | :||||||||.||||||||||||:| |||.||  |||||||||.||::||||||||:|:
Db   119 FLIVLERPEPAQDLFDFITERGALDEPLARRFFRAQVLAAVRHCHSCGVVHRDIKDENLLV 178

Qy   176 DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
           ||:.||||||||||||||||||.|||||||||||||||||||||||||.||||:||||||
Db   179 DLRSGELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy   236 VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM--QDV 293
           ||||||||:||||.||:. ||.||| ||| |||||| |||.:||::::| .|||| :|:
Db   239 VCGDIPFEQDEEILRGRLLFRRRVSPECQOLIRWCLSLRPSERPSLDQIAAHPWMLGADG 298

Qy   294 LLPQETAEIHLHSLSP 309
           ||.|  :|.|:| |.|
Db   299 GAP-ESCDLRICTLDP 313
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RESULT 10
PIM3_MOUSE
ID   PIM3_MOUSE              STANDARD;      PRT;   326 AA.
AC   P58750;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=Pim3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Left column

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RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC  -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC  -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC      subfamily.
CC  -----------------------------------------------------------------------
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----------------------------------------------------------------------
DR  EMBL; BC017621; AAH17621.1; -; mRNA.
DR  EMBL; BC026639; AAH26639.1; -; mRNA.
DR  HSSP; Q03655; 1HOW.
DR  Ensembl; ENSMUSG00000035828; Mus musculus.
DR  MGI; MGI:1355297; Pim3.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR008271; Ser_thr_pkin_AS.
DR  InterPro; IPR002290; Ser_thr_pkinase.
DR  Pfam; PF00069; Pkinase; 1.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00220; S_TKc; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW  ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW  Serine/threonine-protein kinase; Transferase.
FT  DOMAIN    40    293    Protein kinase.
FT  NP_BIND   46     54    ATP (By similarity).
FT  ACT_SITE 170           Proton acceptor (By similarity).
FT  BINDING   69           ATP (By similarity).
SQ  SEQUENCE  326 AA;  35970 MW;  DD68CBF46354851E CRC64;

Query Match             67.6%;
Best Local Similarity   72.2%;
Matches  213;  Conservative  31;  Mismatches  44;  Indels  7;  Gaps  5;
Score 1129.5;  DB 1;  Length 326;

Qy    1 MLLSKINSLAHLRRAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLCGSGGFRGSVYSGIR 57
        |||||.|||.||..||.....||.|||||.||..||||||||||||||||||||||||||||
Db    1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLSSGGFGTVYAGSR   59

Qy   58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLGGGVAVLSGG 115
        ...|||||.||||.|.......||....||.|||||||.||.|||||||||||||||||||
Db   60 IADGLPVAVKHVKERVTEWGSL--GGVAVPLEVVLLRKVGAAGGARGVIRLLDMFERPDG  118

Qy  116 FVILEREPEPVQDLFDFITERGALQEELARSFWQVLEAVRHCHNCGVLHRDIKDENIII 175
        |.|.||||||.|||||||||||||.|.|||.|.|||.||||||||||.|||||||||.||
Db  119 FLIVLEREPEAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV 178

Qy  176 DLNRGELKLIDFGSGALLKDTVTDFDGTRVSSPPEWIRYHRYHGRSAAVWSLGILLLYDM 235
        ||..|||||||||||||.||||.|||||||||||.|||.||||||||||||||||||||||
Db  179 DLRSGELKLIDFGSGAVLKDTVVTDFDGTRVSPPEWIRYHRYHGRSATVWSLGVLLYDM  238

Qy  236 VCGDIPFEHDEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
        |||||||..||.||...|||.|||.||||.|.||||.|||.||..||.||||||
Db  239 VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM 293
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Right column

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RESULT 11
ID  PIM3_RAT     STANDARD;     PRT;   326 AA.
AC  O70444;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  13-SEP-2005 (Rel. 48, Last annotation update)
DE  Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Protein kinase
DE  Kid-1) (Kinase induced by depolarization).
GN  Name=Pim3; Synonyms=Kid1;
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muroidea; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=Sprague-Dawley;
RA  Konietzko U., Kuhl D.;
RT  "Pim-3 is a member of the pim kinase family.";
RL  Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
RN  [2]
RP  NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RX  MEDLINE=98298176; PubMed=9627723; DOI=10.1074/jbc.273.26.16535;
RA  Feldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L.,
RA  Bazan N.G., Baudry M., Herschman H.R.;
RT  "KID-1, a protein kinase induced by depolarization in brain.";
RL  J. Biol. Chem. 273:16535-16543(1998).
CC  -!- INDUCTION: By membrane depolarization or forskolin.
CC  -!- TISSUE SPECIFICITY: Present in a number of unstimulated tissues,
CC      including brain.
CC  -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC  -!- PTM: Autophosphorylated.
CC  -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC      subfamily.
CC  -----------------------------------------------------------------------
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----------------------------------------------------------------------
DR  EMBL; AF086624; AAC68900.1; ALT_INIT; mRNA.
DR  EMBL; AF057026; AAC36065.1; -; mRNA.
DR  HSSP; Q03656; 1HOW.
DR  RGD; 620462; Pim3.
DR  GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR  GO; GO:0046777; P:autophosphorylation; IDA.
DR  GO; GO:0016572; P:histone phosphorylation; IDA.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR008271; Ser_thr_pkin_AS.
DR  InterPro; IPR002290; Ser_thr_pkinase.
DR  Pfam; PF00069; Pkinase; 1.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00220; S_TKc; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW  ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW  Serine/threonine-protein kinase; Transferase.
FT  DOMAIN    40    293    Protein kinase.
FT  NP_BIND   46     54    ATP (By similarity).
FT  ACT_SITE 170           Proton acceptor (By similarity).
FT  BINDING   69           ATP (By similarity).
SQ  SEQUENCE  326 AA;  36002 MW;  DD6C99BF4635F851E CRC64;

Query Match             67.6%;
Best Local Similarity   72.2%;
Matches  213;  Conservative  31;  Mismatches  44;  Indels  7;  Gaps  5;
Score 1128.5;  DB 1;  Length 326;

Qy    1 MLLSKINSLAHLRRAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLCGSGGFRGSVYSGIR 57
        |||||.|||.||..||.....||.|||||.||..||||||||||||||||||||||||||||
Db    1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLSSGGFGTVYAGSR   59

Qy   58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLGGGVAVLSGG 115
        ...|||||.||||.|.......||....||.|||||||.||.|||||||||||||||||||
Db   60 IADGLPVAVKHVKERVTEWGSL--GGMAVPLEVVLLRKVGAAGGARGVIRLLDMFERPDG  118

Qy  116 FVILEREPEPVQDLFDFITERGALQEELARSFWQVLEAVRHCHNCGVLHRDIKDENIII 175
        |.|.||||||.|||||||||||||.|.|||.|.|||.||||||||||.|||||||||.||
Db  119 FLIVLEREPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV 178
```

RESULT 12

```
ID   Q4V8M2_RAT   PRELIMINARY;   PRT;   380 AA.
AC   Q4V8M2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RG   NIH MGC Project;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
     EMBL; BC097317; AAH97317.1; -; mRNA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
FT   NON_TER       1      1
SQ   SEQUENCE   380 AA;  41568 MW;  F82BBE50DD71346 CRC64;

Query Match             67.6%;  Score 1128.5;  DB 2;  Length 380;
  Best Local Similarity   72.2%;  Pred. No. 6.8e-75;
  Matches  213;  Conservative   31;  Mismatches   44;  Indels    7;  Gaps    5;

Qy    176 DLNRGELKLIDFGSGALLKDTVYTDFDFGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
          |||.||||||||||| |:|||||||||||||||||||||||||||||||::||||||:|||
Db    179 DLRSGELKLIDFGGSGAVLKDTVYTDFDFGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy    236 VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRNCLALRPSDRPTFEEIQNHPWM 290
          |||||||:.|||::||::||::||.:||||:||.||:|||.:||::::|..:|||
Db    239 VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM 293
```

RESULT 13

```
ID   Q81X8_MOUSE   PRELIMINARY;   PRT;   325 AA.
AC   Q81X8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GN   Name=Pim3; Synonyms=Kid1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Yu L.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
     EMBL; AY026239; AAK16606.1; -; mRNA.
     HSSP; Q03656; 1Q99.
SMR; Q81X8; 36-292.
MGI; MGI:1355297; Pim3.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   325 AA;  35931 MW;  77DEF8820F41E3F4 CRC64;

Query Match             66.8%;  Score 1116;  DB 2;  Length 325;
  Best Local Similarity   71.9%;  Pred. No. 4.7e-74;
  Matches  212;  Conservative   32;  Mismatches   43;  Indels    8;  Gaps    6;

Qy      1 MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSSGGFGSVYSGIR 57
          ||||| .|||||      |||||| ||||||  |:|||| :|  :|||| |:|| ||:|||
Db      1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQGAVLGSSGGFGTVVAGSR 59

Qy     58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
          ::| |||| ||| |:|  :||:| ||| :  |||||::|  :: :.|::||||||||||.
Db     60 IADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy    116 FVLILERPEPVQDLFDFITERGALQEEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLI 175
          |::||||||||.||||||||||||:|  ||| |  |||:||||||||||||||||||||||:
Db    119 FLIVLERPEPAQDLFDFITERGALDEPLARRFAQVLAAVRHCHNCGVVHRDIKDENLLV 178
```

RESULT 14

PIM3_XENLA

```
Qy  176  DLNRGELKLIDFGSGALLKDTVTFDGTRVSYSPPEWIRYHYRHGRSAAVWSLGILLYDM  235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  179  DLRSGELKLIDFGSGAVLKDTVTFDGTRVSYSPPEWIRYHYRHGRSATVWSLGVLLYDM  238

Qy  236  VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM  290
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  239  VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSRPSDRPSLDKL-CHPWM  292
```

PIM3_XENLA

```
ID   PIM3_XENLA       STANDARD;     PRT;  323 AA.
AC   Q91822;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Pim-1).
GN   Name=PIM3; Synonyms=PIM1;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES.
RX   MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
RA   Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M.,
RA   Aebersold R., Pelech S.L.;
RT   "Identification of the autophosphorylation sites of the Xenopus laevis
RT   Pim-1 proto-oncogene-encoded protein kinase.";
RL   J. Biol. Chem. 272:10514-10521(1997).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -!- CAUTION: Was originally (Ref.1) called Pim-1 but seems to
CC       represent the pim-3 isoform.
-----------------------------------------------------------------------------
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----------------------------------------------------------------------------
DR   EMBL; L29495; AAA85389.1; -; mRNA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation; Transferase;
KW   Serine/threonine-protein kinase.
FT   DOMAIN        40    291       Protein kinase.
FT   NP_BIND       46     54       ATP (By similarity).
FT   ACT_SITE     168    168       Proton acceptor (By similarity).
FT   BINDING       69     69       ATP (By similarity).
FT   BINDING        4      4       Phosphoserine (By similarity)
FT                                 (partial).
FT   MOD_RES      190    190       Phosphoserine (by autocatalysis).
FT   MOD_RES      205    205       Phosphothreonine (by autocatalysis)
FT                                 (partial).
SQ   SEQUENCE   323 AA;  36964 MW;  AB4DD61E7A99A38F CRC64;
```

```
Qy    1  MLLSKINSLAHLRRAAPCN-----DLHATKLAPGK-EKEPLESQVQVGPLLGSGGFGSVYS  54
            ||||| ||| | | |||              |  |  :::   :||:::   :::|||
Db    1  MLLSKFGSLAHI---------CNPSNMEHLPVKILQPVKDKEPFEKYVQVGSVVASGGFGTVYS  56
```

RESULT 15

Q6III1_XENTR

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ID   Q6III1_XENTR PRELIMINARY;     PRT;  318 AA.
AC   Q6III1;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Pim3-prov protein.
GN   Name=pim3-prov;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22382257; PubMed=1477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RL   Klein S., Gerhard D.S.;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC081340; AAH81340.1; -; mRNA.
DR   SMR; Q6III1; 32-297.
DR   Ensembl; ENSXETG00000009354; Xenopus tropicalis.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
```

```
Qy   55  GIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPD  114
            | :|  ||| || |  |  |::|  ||  |  :||:| ||||:|:::|| :||| || |
Db   57  DSRIADGQPVAVKHVAKERVTEWGTL-NGVMVPLEIVLLKKVPAFRGVINLLDWYERPD  115

Qy  115  SFVILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENIL  174
            ||||||:|  ||||||||:||| |:||  :|||||||||||||||||||:|||||||||
Db  116  AFLIVMERPEPVKDLFDYITEKGPLDEDTARGFFRQVLEAVRHCYCNCGVVHRDIKDENLL  175

Qy  175  IDLNRGELKLIDFGSGALLKDTVTFDGTRVSYSPPEWIRYHYRHGRSAAVWSLGILLYDM  234
            ||||||||||||||||| ||||||||||||||||||||||||||||||:|||||:|||||
Db  176  VDTRNGELKLIDFGSGAVLKDTVTFDGTRVSYSPPEWIRYHYRHGRSATVWSLGVLLYD  235

Qy  235  VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM-QDV  293
            |||||||::|||::||:||||:|| |:|| ||  ||| |||||| |::| ||||  |||
Db  236  MVYGDIPFEQDEEIVRVRLCFRRRISTECCQLIKWCLSRPSDRPTLEQIFDHPWMCKCD  295

Qy  294  LLPQETAEIHLHSL  307
            |||| ::|::|:||
Db  296  LVKSEDCDLRLRTI  309
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DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Cell cycle; Cell division; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   318 AA;  36547 MW;  48CCF12797F01FDC CRC64;

Query Match             65.9%;  Score 1101;  DB 2;  Length 318;
Best Local Similarity   70.3%;  Pred. No. 5.9e-73;
Matches  204;  Conservative  38;  Mismatches  38;  Indels  10;  Gaps  4;

Qy         11 HLRAA-PCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHV 69
              ||| : | :|| | |    |||::|:||||||||||:||:::|:||||.:|||||||||
Db         16 HLNSVFPKDDLPAV------KEPFENCYQVGPVIGTGGFGTVYSGVRISDKLPVAIKHV 68

Qy         70 EKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDL 129
              : |||| ||:|||||:|||||| |||||||||||||||||||||:||:||||||:|||
Db         69 SRDRIGEMKHM-NGTLVPLEIYLLKKVSNGCRGVIRLLDWYERPDGFIIIMERPEPVQDL 127

Qy        130 FDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGS 189
              |||||||||| |||||| ||||||||||:||:  |||||||||||||:||||||||||||
Db        128 FDFITERGALGEELATNFFRQVVEAVRHCHSCDVVHRDIKDENILVDLRTAELKLIDFGS 187

Qy        190 GALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEII 249
              |||| |:|||||||||||||||||||||:||||:|||||||||||||||||||||:| :
Db        188 GALLRDAVYTDFDGTRVYSPPEWIRFHXYHGRSATVWSLGILLYDMVCGDIPFEHDDEIL 247

Qy        250 RGQVFRQRVSSECQQHLIRWCLALRPSDRPTFEEIQNHPWM-QDVLLPQE 298
              ||:||:|||| |||||||||||| :: | ||||||  ||||||| ||| ||
Db        248 KGKIQYRCRVSRECQHLIEWCLSKRPSDRPSLEQILAHPWMSQDNFLDKK 297
```

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: May 4, 2006, 05:25:14 ; Search time 28.6667 Seconds
                 (without alignments)
                 902.703 Million cell updates/sec

Title: US-10-705-757-4
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRAAPCNDL...........LLPQATAEIHLHSLSPSPSK 313

Scoring table: BLOSUM62
Scoring: Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters: 572060

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1668	100.0	313	2	US-09-237-543-8	Sequence 8, Appli
2	1668	100.0	313	2	US-09-644-450-8	Sequence 8, Appli
3	1636	98.1	313	2	US-09-237-543-9	Sequence 9, Appli
4	1636	98.0	313	2	US-09-644-450-9	Sequence 9, Appli
5	1623	97.3	313	1	US-08-463-081B-26	Sequence 26, Appl
6	1623	97.3	313	1	US-08-461-379A-26	Sequence 26, Appli
7	1623	97.3	313	1	US-08-462-390B-26	Sequence 26, Appl
8	1623	97.3	313	1	US-08-463-074B-26	Sequence 26, Appl
9	1623	97.3	313	2	US-08-465-585C-26	Sequence 26, Appl
10	1623	97.3	313	2	US-08-652-44-26	Sequence 26, Appl
11	1584	95.0	313	2	US-09-237-543-7	Sequence 7, Appli
12	1584	95.0	313	2	US-09-644-450-7	Sequence 7, Appli
13	1304.5	78.2	257	1	US-07-857-224B-41	Sequence 41, Appl
14	1135	68.0	326	2	US-09-237-543-2	Sequence 2, Appli
15	1135	67.8	326	2	US-09-644-450-2	Sequence 2, Appli
16	1131.5	67.8	455	2	US-09-237-543-5	Sequence 5, Appli
17	1131.5	67.8	455	2	US-09-644-450-5	Sequence 5, Appli
18	1102.5	66.1	323	2	US-09-237-543-6	Sequence 6, Appli
19	1102.5	66.1	323	2	US-09-644-450-6	Sequence 6, Appli
20	1083.5	65.0	254	2	US-09-237-543-4	Sequence 4, Appli
21	1083.5	65.0	254	2	US-09-644-450-4	Sequence 4, Appli
22	866.5	51.9	311	2	US-10-184-563-2	Sequence 2, Appli
23	866.5	51.9	372	2	US-09-949-016-7140	Sequence 7140, Ap
24	378.5	22.7	256	2	US-09-964-956-74	Sequence 74, Appl
25	376.5	22.6	778	2	US-10-116-326-2	Sequence 2, Appli
26	376.5	22.6	778	2	US-10-003-690-2	Sequence 2, Appli
27	376.5	22.6	778	2	US-10-803-277-2	Sequence 2, Appli
28	374	22.4	1101	2	US-09-770-170-8	Sequence 8, Appli
29	370.5	22.2	776	2	US-09-523-849-34	Sequence 34, Appl
30	366	22.2	1356	2	US-09-770-170-6	Sequence 6, Appli
31	364.5	21.9	630	2	US-10-355-975A-38	Sequence 38, Appl
32	364.5	21.9	631	2	US-09-579-664B-11	Sequence 11, Appl
33	364.5	21.9	631	2	US-10-355-975A-11	Sequence 11, Appl
34	363.5	21.8	1323	2	US-09-770-170-2	Sequence 2, Appli
35	357.5	21.4	668	2	US-09-930-181-2	Sequence 2, Appli
36	357.5	21.4	668	2	US-10-054-579-2	Sequence 2, Appli
37	357.5	21.4	674	2	US-10-283-247-2	Sequence 2, Appli
38	357	21.4	512	2	US-09-633-328B-4	Sequence 4, Appli
39	356	21.3	256	2	US-09-633-328B-2	Sequence 2, Appli
40	355.5	21.3	281	2	US-09-248-796A-20512	Sequence 20512, A
41	353.5	21.2	674	2	US-10-283-247-7	Sequence 7, Appl
42	353.5	21.2	674	2	US-09-964-956-72	Sequence 72, Appl
43	353.5	21.2	674	2	US-10-283-247-8	Sequence 8, Appli
44	343.5	20.6	722	2	US-08-817-832B-32	Sequence 32, Appl
45	343	20.6	1005	2	US-09-770-170-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-237-543-8
; Sequence 8, Application US/0923754A3
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-8

Query Match   100.0%; Score 1668; DB 2; Length 313;
Best Local Similarity   100.0%; Pred. No. 1.4e-164;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGGFGSVYSGIRVAD 60
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Db    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILILDLNRG 180
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Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILILDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVVTDFDGTRVVSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  181 ELKLIDFGSGALLKDTVVTDFDGTRVVSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECCHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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Db  241 PFEHDEEIVKGQVYFRQRVSSECCHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPSPSK 313
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Db  301 EIHLHSLSPSPSK 313
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RESULT 2
US-09-644-450-8

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; Sequence 8, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 03580D/175631
;   CURRENT APPLICATION NUMBER: US/09/644,450
;   CURRENT FILING DATE: 2000-08-23
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-644-450-8

Query Match             100.0%;  Score 1668;  DB 2;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 1.4e-164;
Matches 313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPSPSK 313
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Db  301 EIHLHSLSPSPSK 313

RESULT 3
US-09-237-543-9
; Sequence 9, Application US/0923754343A
; Patent No. 6143540
; GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   FILE REFERENCE: 03580D/175631
;   CURRENT APPLICATION NUMBER: US/09/237,543A
;   CURRENT FILING DATE: 1999-01-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-237-543-9

Query Match             98.1%;  Score 1636;  DB 2;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 3e-161;
Matches 304;  Conservative  6;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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RESULT 4
US-09-644-450-9
; Sequence 9, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 03580D/175631
;   CURRENT APPLICATION NUMBER: US/09/644,450
;   CURRENT FILING DATE: 2000-08-23
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-644-450-9

Query Match             98.1%;  Score 1636;  DB 2;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 3e-161;
Matches 304;  Conservative  6;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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Db    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPSPSK 313

RESULT 5
US-08-463-081B-26
; Sequence 26, Application US/08463081B
; Patent No. 5871960
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Patent No. 5871960 5837487
GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,081B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: amino acid
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-463-081B-26

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Query Match    97.3%; Score 1623; DB 1; Length 313;
Best Local Similarity   96.5%; Pred. No. 6.7e-160;
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Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGFGSGVYSGIRVAD 60
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Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db  121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313
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RESULT 6
US-08-461-379A-26
; Sequence 26, Application US/08461379A
; Patent No. 5871961
GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; ADDRESSEE: (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,379A
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108; 08/104,736
; APPLICATION NUMBER: & 07/796,066
; FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: DART-070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)470-0700
; TELEFAX: (610)470-0701
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-461-379A-26

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Query Match    97.3%; Score 1623; DB 1; Length 313;
Best Local Similarity   96.5%; Pred. No. 6.7e-160;
Matches  302; Conservative   6; Mismatches   5; Indels   0; Gaps   0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGFGSGVYSGIRVAD 60
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Db    1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSGVYSGIRVSD 60

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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db  121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

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Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313
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RESULT 7
US-08-462-390B-26
; Sequence 26, Application US/08462390B
; Patent No. 5882894
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A.; & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,390B
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: USSN 08/104,736
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: USSN 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: DART-040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)407-0700
; TELEFAX: (610)407-0701
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-462-390B-26

Query Match   97.3%; Score 1623; DB 1; Length 313;
Best Local Similarity   96.5%; Pred. No. 6.7e-160;
Matches 302; Conservative   6; Mismatches   5; Indels   0; Gaps   0;

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Qy     1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
           ||||||| : || |||||||||||||||||| ||||||| ||||||||||||||||| ||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPSPSK 313
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Db   301 EIHLHSLSPGPSK 313
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RESULT 8
US-08-463-074B-26
; Sequence 26, Application US/08463074B
; Patent No. 6020155
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein, Vector an
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; (B) STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,074B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; SOFTWARE: PatentIn Release #1.0,
; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-463-074B-26

Query Match   97.3%; Score 1623; DB 2; Length 313;
Best Local Similarity   96.5%; Pred. No. 6.7e-160;
Matches 302; Conservative   6; Mismatches   5; Indels   0; Gaps   0;

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Qy     1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
           ||||||||||||| |: |||||| |||||||||||||||||||||||||||| ||||| |
Db     1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVVSGIRVSD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
           ||||||| : || |||||||||||||||||| ||||||| ||||||||||||||||| ||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPSPSK 313
           |||||||| ||||
Db   301 EIHLHSLSPGPSK 313
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; Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
; ||||||||||||:|||:||||||||||||||||||||:||||||||||||||||||| ||
; Qy   301 EIHLHSLSPGPSK 313
; |||||||||||||
; Db   301 EIHLHSLSPGPSK 313

RESULT 9
US-08-465-585C-26
; Patent No. 6027914
; Sequence 26, Application US/08465585C
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A., & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
;   ADDRESSEE: (B) STREET: 444South Flower St. - Suite 190
;   CITY: Los Angeles
;   STATE: Californiaa
;   COUNTRY: USA
;   ZIP: 900071
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/465,585C
;   FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/330,108
;   FILING DATE: 27-OCT-1994
;   APPLICATION NUMBER: USSN 08/104,736
;   FILING DATE: 10-AUG-1993
;   APPLICATION NUMBER: USSN 07/796,066
;   FILING DATE: 20-NOV-1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: Viviana Amzel, Ph. D.
;   REGISTRATION NUMBER: 30,930
;   REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (213) 622-7700
;   TELEFAX: (213) 484210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 313 amino acids
;   TYPE: peptide
;   STRANDEDNESS: n.a.
;   TOPOLOGY: n.a.
; MOLECULE TYPE: peptide

  Query Match   97.3%; Score 1623; DB 2; Length 313;
  Best Local Similarity   96.5%; Pred. No. 6.7e-160;
  Matches 302; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD   60
             |||||||||||||| |||||||:|||||||||||||||||||||||||||||||||||:|
Db   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVSD   60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120

Qy   121 ERPEPVQDLFDIITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
             ||:||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERREPVQDLFDITTERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDFGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDFGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVRGQVFFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
             ||||||||:|||||||||||||||||||||||:||||||:|||||||||||||||||||| ||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
             |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 10
US-08-652-446-26
; Sequence 26, Application US/08652446
; Patent No. 6057427
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide, Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
;   ADDRESSEE: (B) STREET: 444 South Flower St. - Suite 190
;   CITY: Los Angeles
;   STATE: California
;   COUNTRY: USA
;   ZIP: 90071
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/652,446
;   FILING DATE:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/330,108
;   FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP App. # 96921319.8
;   FILING DATE: 5-JAN-1998
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US/96/09194
;   FILING DATE: 5-JUN-1996
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/330,108
;   FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/462,390
;   FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/462,337
;   FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/463,074
;   FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/465,585
;   FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/463,081
;   FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/461,379
;   FILING DATE: 5-JUN-1991
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/739,523
;   FILING DATE: 29-OCT-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Viviana Amzel, Ph. D.
;   REGISTRATION NUMBER: 30,930
;   REFERENCE/DOCKET NUMBER: P66 40035
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (213) 622-7700
;   TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:

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  SEQUENCE CHARACTERISTICS:
;   LENGTH: 313 amino acids
;   TYPE: peptide
;   STRANDEDNESS: n.a.
;   TOPOLOGY: n.a.
;   MOLECULE TYPE: peptide
US-08-652-446-26

Query Match             97.3%;  Score 1623;  DB 2;  Length 313;
Best Local Similarity   96.5%;  Pred. No. 6.7e-160;
Matches 302;  Conservative  6;  Mismatches  5;  Indels  0;  Gaps  0;

Qy          1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              ||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVIIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVIIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPMMQDVLLPQATA 300
              |||||||||||||||||||||||||:|||||||||||||||||||||||||:||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy        301 EIHLHSLSPSPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313

RESULT 11
US-09-237-543-7
; Sequence 7, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/237,543A
;   CURRENT FILING DATE: 1999-01-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 7
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-237-543-7

Query Match             95.0%;  Score 1584;  DB 2;  Length 313;
Best Local Similarity   94.2%;  Pred. No. 7.5e-156;
Matches 295;  Conservative  8;  Mismatches 10;  Indels  0;  Gaps  0;

Qy          1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVIIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSDFSGVIRLLDWFERPDSFVIIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||:|
Db        121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPMMQDVLLPQATA 300
              |||||||||||||||||||||||||:||||||||||||||:||||||||||||||||||:
Db        241 PFEHDEEIIKGQVFFRQRVSSECQHLIRWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS 300

Qy        301 EIHLHSLSPSPSK 313
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Db        301 EIHLHSLSPGSSK 313

RESULT 12
US-09-644-450-7
; Sequence 7, Application US/09644450
; Patent No. 6387791
; GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/644,450
;   CURRENT FILING DATE: 2000-08-23
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 7
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-644-450-7

Query Match             95.0%;  Score 1584;  DB 2;  Length 313;
Best Local Similarity   94.2%;  Pred. No. 7.5e-156;
Matches 295;  Conservative  8;  Mismatches 10;  Indels  0;  Gaps  0;

Qy          1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVIIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSDFSGVIRLLDWFERPDSFVIIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||:|
Db        121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPMMQDVLLPQATA 300
              |||||||||||||||||||||||||:||||||||||||||:||||||||||||||||||:
Db        241 PFEHDEEIIKGQVFFRQRVSSECQHLIRWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS 300

Qy        301 EIHLHSLSPSPSK 313
              |||||||||| ||
Db        301 EIHLHSLSPGSSK 313

RESULT 13
US-07-857-224B-41
; Sequence 41, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
;   APPLICANT: Benner, Steven A.
;   TITLE OF INVENTION: Predicting Folded Structures of Proteins
;   NUMBER OF SEQUENCES: 114
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Steven A. Benner
;     STREET: Hadlaubstrasse 151
;     CITY: Zurich
;     STATE: none
```

```
;   COUNTRY: Switzerland
;   ZIP: (note: this is an international post code) CH-8092
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
;   COMPUTER: Apple Macintosh
;   OPERATING SYSTEM: Macintosh 7.0
;   SOFTWARE: Microsoft Word
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/857,224B
;   FILING DATE: 03/25/92
;   CLASSIFICATION: 436
;   PRIOR APPLICATION DATA: none
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (International) 41 1 632 2830
;   TELEFAX: (International) 41 1 262 2437
;   TELEX: none
;   INFORMATION FOR SEQ ID NO: 41:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 257
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   DESCRIPTION: protein
;   ORIGINAL SOURCE:
;   ORGANISM: rat
;   FEATURE: Protein kinase; Table 8 Column 46
;   PUBLICATION INFORMATION:
;   AUTHORS: Hanks, S. K.
;   AUTHORS: Quinn, A. M.
;   AUTHORS: Hunter, T.
;   TITLE: The protein kinase family
;   JOURNAL: Science
;   VOLUME: 241
;   PAGES: 42-52
;   DATE: 1988
;   US-07-857-224B-41

Query Match         78.2%;   Score 1304.5;  DB 1;  Length 257;
Best Local Similarity   94.9%;  Pred. No. 5.6e-127;
Matches  244;  Conservative  7;  Mismatches  3;  Indels  3;  Gaps  2;

Qy  36  SOYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKK  95
        |||||||||||||||||||||||||||||||||||||||||||   |||||||||||||
Db   1  SOYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGE--NGTRVPMEVVLLKK  58

Qy  96  VSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAV  155
        ||| ||||||||||||||| ||||||||||||||||||||||||||:||| |||||||||
Db  59  VSSDFSGVIRLLDWFERDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAV  118

Qy 156  RICHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVTYDFDGTRVSYSPPEWIRY  215
        ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db 119  RICHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVTFDFDGTRVRYSPPEWIRY  178

Qy 216  HRYHGRSAAVWSLGILLYDMVCGDIPF-EHDEEIVKGQVYFRQRVSSECQHLIRWCLSLR  274
        |||||||||||||||||||||||||||  |||||:|||||:|||:|||||||||||||||
Db 179  HRYHGRSAAVWSLGILLYDMVCGDIPFDEHDEEIIKGQVFFRQTVSSECQHLIRWCLSLR  238

Qy 275  PSDRPSFEEIQNHPWMQ  291
        ||||||||||:||||||
Db 239  PSDRPSFEEIRNHPWMQ  255

RESULT 14
US-09-237-543-2
;   Sequence 2, Application US/09237543A
;   Patent No. 6143540
;   GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/237,543A
;   CURRENT FILING DATE: 1999-01-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 2
;   LENGTH: 326
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-237-543-2

Query Match         68.0%;   Score 1135;  DB 2;  Length 326;
Best Local Similarity   69.6%;  Pred. No. 3.1e-109;
Matches  220;  Conservative  34;  Mismatches  52;  Indels  10;  Gaps  7;

Qy   1  MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR  57
        |||| : |||:||:||    :|| |   |||| |:|||:||:|||||||||||||||||:
Db   1  MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGPLLGSGGFGSVYYAGSR  59

Qy  58  VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS  115
        ||| ||||:|:|:|| :|||| | |||||:|||||||:|  :||||||||||||||||||
Db  60  IADGLPVAVHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG  118

Qy 116  FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI  175
        | ||||||||:|||||||||||||:| ||| ||:|||:|||||||:|||:|||||||:||:
Db 119  FLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV  178

Qy 176  DLNRGELKLIDFGSGALLKDTVTYDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDM  235
        ||  |||||||||||||||||||:|||||||| ||||||||||||||||:||||||:||||
Db 179  DLRSGELKLIDFGSGALLKDTVTFDFDGTRVRYSPPEWIRYHRYHGRSATVWSLGVLLYDM  238

Qy 236  VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRSDRPSFEEIQNHPWM--QDV  293
        ||||||| || ||:|| :| |:|||:|||||||||||||| :| ||:  |||||   ||
Db 239  VCGDIPFEQDEEILRGRLFRRRVSPECQHLIRWCLSLRPSERPSLDQIAAHPWMLGADG  298

Qy 294  LLPQATAEIHLHSLSP  309
        |:|: ||||| |||:|
Db 299  GAPE-SCDLRLCTLDP  313

RESULT 15
US-09-644-450-2
;   Sequence 2, Application US/09644450
;   Patent No. 6383791
;   GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/644,450
;   CURRENT FILING DATE: 2000-08-23
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 2
;   LENGTH: 326
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-644-450-2

Query Match         68.0%;   Score 1135;  DB 2;  Length 326;
Best Local Similarity   69.6%;  Pred. No. 3.1e-109;
Matches  220;  Conservative  34;  Mismatches  52;  Indels  10;  Gaps  7;

Qy   1  MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR  57
        |||| : |||:||:||    :|| |   |||| |:|||:||:|||||||||||||||||:
Db   1  MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGPLLGSGGFGSVYYAGSR  59

Qy  58  VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS  115
        ||| ||||:|:|:|| :|||| | |||||:|||||||:|  :||||||||||||||||||
Db  60  IADGLPVAVHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG  118

Qy 116  FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI  175
        | ||||||||:|||||||||||||:| ||| ||:|||:|||||||:|||:|||||||:||:
Db 119  FLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV  178
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Qy  176  DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM  235
              || |||||||||||||||||||||||||||||||||||||||||:|||||||||:||||
Db  179  DLRSGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM  238

Qy  236  VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM--QDV  293
              |||||||:||||: ::  | ::| ::|||:||||||||||:|||: :  ||||  |
Db  239  VCGDIPFEQDEEILRGRLLFRRRVSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADG  298

Qy  294  LLPQATAEIHLHSLSP  309
              |: :|  :|:|:|
Db  299  GAPE-SCDLRLCTLDP  313
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OM protein - protein search, using sw model

Copyright (c) 1993 - 2006 Bioacceleration Ltd.   GenCore version 5.1.7

Run on: May 4, 2006, 05:26:13 ; Search time 92.6667 Seconds
                              (without alignments)
                              1411.301 Million cell updates/sec

Title: US-10-705-757-4
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRAAPCNDL.........LLPQATAEIHLHSLSPSPSK 313

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
             1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
             2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
             3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
             4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
             5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
             6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1668	100.0	313	3	US-09-971-791-8	Sequence 8, Appli
2	1668	100.0	313	4	US-10-425-114-54275	Sequence 54275, A
3	1668	100.0	313	4	US-09-971-791-2	Sequence 2, Appli
4	1636	98.1	313	3	US-10-705-757-9	Sequence 9, Appli
5	1636	98.1	313	4	US-09-971-791-9	Sequence 9, Appli
6	1636	98.1	313	4	US-10-081-119-18	Sequence 18, Appl
7	1636	98.1	313	4	US-10-394-322A-52	Sequence 52, Appl
8	1636	98.1	313	4	US-10-348-081-13	Sequence 13, Appl
9	1636	98.1	313	4	US-10-664-421-1	Sequence 1, Appl
10	1636	98.1	313	4	US-10-664-421-150	Sequence 150, App
11	1636	98.1	313	4	US-10-705-757-2	Sequence 2, Appl
12	1636	98.1	313	4	US-10-377-268-9	Sequence 9, Appli
13	1636	98.1	313	5	US-10-951-389-18	Sequence 18, Appl
14	1636	98.1	313	5	US-10-951-406-18	Sequence 18, Appl
15	1636	98.1	313	5	US-10-951-477-18	Sequence 18, Appl
16	1636	98.1	313	5	US-10-977-087-18	Sequence 18, Appl
17	1636	98.1	313	5	US-10-941-635-152	Sequence 152, App
18	1623	97.3	313	5	US-10-620-052A-22	Sequence 22, Appl
19	1584	95.0	313	4	US-09-971-791-7	Sequence 7, Appli
20	1584	95.0	313	4	US-10-348-081-14	Sequence 14, Appl
21	1584	95.0	313	4	US-10-705-757-6	Sequence 6, Appli
22	1584	95.0	313	4	US-10-377-268-10	Sequence 10, Appl
23	1584	95.0	253	5	US-10-941-635-2	Sequence 2, Appli
24	1584	95.0	253	4	US-10-620-052A-71	Sequence 71, Appli
25	1345	80.5	323	4	US-10-664-421-7	Sequence 7, Appli
26	1137	68.2	323	4	US-10-377-268-15	Sequence 15, Appli
27	1137	68.2	323	4	US-10-377-268-15	Sequence 15, Appli
28	1137	68.2	323	5	US-10-941-635-7	Sequence 7, Appli
29	1137	68.2	374	4	US-10-425-114-54275	Sequence 54275, A
30	1135	68.0	326	3	US-09-971-791-2	Sequence 2, Appli
31	1135	68.0	326	4	US-10-348-081-2	Sequence 2, Appli
32	1135	68.0	326	4	US-10-664-421-166	Sequence 166, App
33	1135	68.0	326	4	US-10-618-941-82	Sequence 82, Appl
34	1135	68.0	374	4	US-10-425-114-54264	Sequence 54264, A
35	1132.5	67.9	326	4	US-10-348-081-6	Sequence 6, Appli
36	1132.5	67.9	326	4	US-10-705-757-11	Sequence 11, Appl
37	1132.5	67.9	326	4	US-10-377-268-14	Sequence 14, Appl
38	1132.5	67.9	326	5	US-10-941-635-6	Sequence 6, Appli
39	1131.5	67.8	326	4	US-10-348-081-10	Sequence 10, Appl
40	1131.5	67.8	455	4	US-09-971-791-5	Sequence 5, Appli
41	1131.5	67.8	455	4	US-10-664-421-1	Sequence 1, Appli
42	1119	67.1	323	4	US-09-971-791-6	Sequence 6, Appli
43	1102.5	66.1	323	3	US-10-348-081-11	Sequence 11, Appl
44	1102.5	66.1	323	4	US-10-664-421-8	Sequence 8, Appli
45	1102.5	66.1	323	4	US-10-664-421-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-971-791-8
; Sequence 8, Application US/09971791
; Patent No. US2002011512OA1
; GENERAL INFORMATION:
;   APPLICANT: Rosanna Kapeller-Libermann
;   APPLICANT: Laura A. Rudolph-Owen
;   APPLICANT: Kyle MacBeth
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES T:
;   FILE REFERENCE: 35800/238856
;   CURRENT APPLICATION NUMBER: US/09/971,791
;   CURRENT FILING DATE: 2001-10-04
;   PRIOR APPLICATION NUMBER: 09/644,450
;   PRIOR FILING DATE: 2000-08-23
;   PRIOR APPLICATION NUMBER: 09/237,543
;   PRIOR FILING DATE: 1999-01-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-971-791-8

Query Match   100.0%; Score 1668; DB 3; Length 313;
Best Local Similarity   100.0%; Pred. No. 5.8e-143;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy         1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db         1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy        61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy       121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy       181 ELKLIDFGSGALLKDTVYTFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 ELKLIDFGSGALLKDTVYTFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy       241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy       301 EIHLHSLSPSPSK 313
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Db       301 EIHLHSLSPSPSK 313
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Db   301 EIHLHSLSPSPSK 313

RESULT 2
US-10-348-081-12
Sequence 12, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: KORN, Marcus
; APPLICANT: MUELLER, Guenter
; APPLICANT: SCHNEIDER, Rudolf
; APPLICANT: TSCHANK, Georg
; TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: DEAV2002/0004 US NP
; CURRENT APPLICATION NUMBER: US/10/348,081
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 12
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus

US-10-348-081-12

Query Match   100.0%; Score 1668; DB 4; Length 313;
Best Local Similarity   100.0%; Pred. No. 5.8e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy 301 EIHLHSLSPSPSK 313
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Db 301 EIHLHSLSPSPSK 313

RESULT 3
US-10-705-757-4
Sequence 4, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
; APPLICANT: GRUENENTHAL GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCE: 029310.5281BUS
; CURRENT APPLICATION NUMBER: US/10/705,757
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus

US-10-705-757-4

Query Match   100.0%; Score 1668; DB 4; Length 313;
Best Local Similarity   100.0%; Pred. No. 5.8e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
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Db 181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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Db 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy 301 EIHLHSLSPSPSK 313
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Db 301 EIHLHSLSPSPSK 313

RESULT 4
US-09-971-791-9
Sequence 9, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THE
; FILE REFERENCE: 35800/2338856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-971-791-9

Query Match   98.1%; Score 1636; DB 3; Length 313;
Best Local Similarity   97.1%; Pred. No. 4.7e-140;
Matches 304; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240

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Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPSPSK 313
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Db  301 EIHLHSLSPGPSK 313
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RESULT 5
US-10-081-119-18
; Sequence 18, Application US/10081119
; Publication No. US20030045491A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/081,119
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-119-18

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Query Match             98.1%;  Score 1636;  DB 4;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 4.7e-140;
Matches  304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVAD 60
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Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPSPSK 313
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Db  301 EIHLHSLSPGPSK 313
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RESULT 6
US-10-394-322A-52
; Sequence 52, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A

; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-52

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Query Match             98.1%;  Score 1636;  DB 4;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 4.7e-140;
Matches  304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVAD 60
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Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||| :|||||||||||||||||| ||||||| |||||||||||||||||| ||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPSPSK 313
        |||||||| |||
Db  301 EIHLHSLSPGPSK 313
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RESULT 7
US-10-348-081-13
; Sequence 13, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: KORN, Marcus
; APPLICANT: MUELLER, Guenter
; APPLICANT: SCHNEIDER, Rudolf
; APPLICANT: TSCHANK, Georg
; TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: DEAV2002/0004 US NP
; CURRENT APPLICATION NUMBER: US/10/348,081
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 13
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-081-13

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Query Match             98.1%;  Score 1636;  DB 4;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 4.7e-140;
Matches  304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVAD 60
        |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        |||||||:|:||||||||||||:||||||:||||||:|||||||||||||||||||:||
Db  241 PFEHDEEIIRGQVFFRQRVSSECCHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPSPSK 313
        ||||||||| |||
Db  301 EIHLHSLSPGPSK 313
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RESULT 8
US-10-664-421-1

; Sequence 1, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
;
; SEQ ID NO 1
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-1

  Query Match   98.1%; Score 1636; DB 4; Length 313;
  Best Local Similarity   97.1%; Pred. No. 4.7e-140;
  Matches 304; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        |||||||||||||||||||||:|||||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        |||||||:|:||||||||||||:||||||:||||||:|||||||||||||||||||:||
Db  241 PFEHDEEIIRGQVFFRQRVSSECCHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPSPSK 313
        ||||||||| |||
Db  301 EIHLHSLSPGPSK 313
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RESULT 9

US-10-664-421-150
; Sequence 150, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
;
; SEQ ID NO 150
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-150

  Query Match   98.1%; Score 1636; DB 4; Length 313;
  Best Local Similarity   97.1%; Pred. No. 4.7e-140;
  Matches 304; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
        |||||||||||||||||||||:|||||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECCHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        |||||||:|:||||||||||||:||||||:||||||:|||||||||||||||||||:||
Db  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPSPSK 313
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RESULT 10
US-10-705-757-2
; Sequence 2, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
; APPLICANT: GRUENENTHAL GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCE: 029910.5281BUS
; CURRENT APPLICATION NUMBER: US/10/705,757
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-705-757-2

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Query Match      98.1%;  Score 1636;  DB 4;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 4.7e-140;
Matches  304;  Conservative  6;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||:| ||:|||||||||||||||:|||||||:||||||||||||||||:|| ||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
        |||||||| |||
Db  301 EIHLHSLSPGPSK 313
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RESULT 11
US-10-377-268-9
; Sequence 9, Application US/10377268
; Publication No. US20040171062A1
; GENERAL INFORMATION:
; APPLICANT: HIRTH, KLAUS-PETER
; APPLICANT: MILBURN, MICHAEL VANCE
; TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
; FILE REFERENCE: 039363/0303
; CURRENT APPLICATION NUMBER: US/10/377,268
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: 60/437,929
; PRIOR APPLICATION FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/360,651
; PRIOR APPLICATION FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR APPLICATION FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR APPLICATION FILING DATE: 2002-09-20
; SOFTWARE: Patentin Ver. 2.1
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-377-268-9

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Query Match      98.1%;  Score 1636;  DB 4;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 4.7e-140;
Matches  304;  Conservative  6;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||:| ||:|||||||||||||||:|||||||:||||||||||||||||:|| ||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
        |||||||| |||
Db  301 EIHLHSLSPGPSK 313
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RESULT 12
US-10-951-389-18
; Sequence 18, Application US/10951389
; Publication No. US20050058627A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,389
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR APPLICATION FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR APPLICATION FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-389-18

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Query Match      98.1%;  Score 1636;  DB 5;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 4.7e-140;
Matches  304;  Conservative  6;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||:| ||:|||||||||||||||:|||||||:||||||||||||||||:|| ||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
        ||||||||| |||
Db  301 EIHLHSLSPGPSK 313
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RESULT 13
US-10-951-406-18
; Sequence 18, Application US/10951406
; Publication No. US20050059630A1

; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,406
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-951-406-18

Query Match   98.1%;   Score 1636;   DB 5;   Length 313;
Best Local Similarity   97.1%;   Pred. No. 4.7e-140;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGFPGSVYSGIRVAD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFPGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy   301 EIHLHSLSPSPSK 313
           ||||||||||||
Db   301 EIHLHSLSPGPSK 313

US-10-951-477-18

RESULT 14
US-10-951-477-18
Sequence 18, Application US/10951477
; Publication No. US20050063974A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,477
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-951-477-18

Query Match   98.1%;   Score 1636;   DB 5;   Length 313;
Best Local Similarity   97.1%;   Pred. No. 4.7e-140;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGFPGSVYSGIRVAD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFPGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy   301 EIHLHSLSPSPSK 313
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Db   301 EIHLHSLSPGPSK 313

RESULT 15
US-10-977-087-18
Sequence 18, Application US/10977087
; Publication No. US20050130926A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xin, Hong
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Khoja, Hamiduddin
; APPLICANT: Shyamala, Venkatakrishna
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS
; TITLE OF INVENTION: CELLS AND THEIR METHODS OF USE V
; FILE REFERENCE: 2300-21986
; CURRENT APPLICATION NUMBER: US/10/977,087
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: 10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/271,254
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 10/360,848
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: 09/570,593
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 10/763,692
; PRIOR FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: 09/626,301
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/148,936
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/145,612
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 10/698,959
; PRIOR FILING DATE: 2003-10-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 18

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;  LENGTH: 313
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-977-087-18

Query Match      98.1%;   Score 1636;   DB 5;   Length 313;
Best Local Similarity   97.1%;   Pred. No. 4.7e-140;
Matches  304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy     1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVAD 60
         ||||||||||||||||||:|||||||||||||||||||||||||||||||||||:|
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITTERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITTERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPSPSK 313
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Db   301 EIHLHSLSPGPSK 313
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OM protein - protein search, using sw model

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GenCore version 5.1.7

Run on: May 4, 2006, 05:27:44 ; Search time 15.3333 Seconds
                 944.812 Million cell updates/sec
                 (without alignments)

Title: US-10-705-757-4
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRAAPCNDL..........LLPQATAEIHLHSLSPSPSK 313

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA New:*
                 1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep1:*
                 2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 4: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 5: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 6: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 7: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 8: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 9: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1:*
                10: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                11: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                12: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1131.5	67.8	455	9	US-10-784-004-373	Sequence 373, App
2	869	52.1	334	8	US-10-511-937-2982	Sequence 2982, Ap
3	869	52.1	334	8	US-10-501-841-32	Sequence 32, Appl
4	866.5	51.9	311	9	US-10-501-841-40	Sequence 40, Appl
5	866.5	51.9	311	11	US-11-103-065-2	Sequence 2, Appli
6	381.5	22.9	661	8	US-10-105-928-690	Sequence 690, App
7	378.5	22.7	256	9	US-10-877-346-74	Sequence 74, Appl
8	367	22.0	504	11	US-11-087-099-9816	Sequence 9816, Ap
9	367	22.0	950	9	US-10-501-035-357	Sequence 357, App
10	364.5	21.9	631	11	US-11-241-056-11	Sequence 11, Appl
11	358	21.5	514	11	US-11-087-099-11500	Sequence 11500, A
12	355.5	21.3	256	9	US-10-877-346-72	Sequence 72, Appl
13	355.5	21.3	256	11	US-11-113-424-183	Sequence 183, App
14	350.5	21.0	504	11	US-11-087-099-12331	Sequence 12331, A
15	350	21.0	512	11	US-11-087-099-3997	Sequence 3997, Ap
16	350	21.0	514	11	US-11-087-099-3612	Sequence 3612, Ap
17	348	20.9	472	11	US-11-087-099-11838	Sequence 11838, A
18	346	20.7	86	9	US-10-501-841-37	Sequence 37, Appl
19	346	20.7	464	11	US-11-087-099-22124	Sequence 22124, A
20	344	20.6	513	11	US-11-087-099-11726	Sequence 11726, A
21	342.5	20.5	722	9	US-10-784-004-435	Sequence 435, App
22	342.5	20.5	722	9	US-10-784-004-951	Sequence 951, App
23	340.5	20.4	651	9	US-10-770-726-67	Sequence 67, Appl
24	340.5	20.4	651	11	US-11-177-138-10	Sequence 10, Appl
25	338.5	20.3	619	11	US-11-087-099-12402	Sequence 12402, A
26	338	20.3	713	9	US-10-995-561-881	Sequence 881, App
27	338	20.3	729	9	US-10-995-561-878	Sequence 878, App
28	338	20.3	737	9	US-10-995-561-880	Sequence 880, App
29	338	20.3	744	9	US-10-995-561-876	Sequence 876, App
30	338	20.3	753	9	US-10-995-561-877	Sequence 877, App
31	336.5	20.2	445	11	US-11-096-568A-32575	Sequence 32575, A
32	335.5	20.1	689	9	US-10-204-639-17	Sequence 17, Appl
33	334.5	20.1	651	11	US-11-087-099-11886	Sequence 1886, Ap
34	333.5	20.0	715	9	US-10-204-639-65	Sequence 65, Appl
35	332	19.9	620	11	US-11-087-099-3898	Sequence 3898, Ap
36	331.5	19.9	358	9	US-10-979-095-6	Sequence 6, Appli
37	329.5	19.8	448	11	US-11-096-568A-18364	Sequence 18364, A
38	327	19.6	516	11	US-11-087-099-1845	Sequence 1845, Ap
39	325.5	19.5	439	11	US-11-096-568A-20431	Sequence 20431, A
40	325.5	19.5	443	11	US-11-096-568A-20430	Sequence 20430, A
41	325	19.5	277	11	US-11-151-601-4	Sequence 4, Appli
42	325	19.5	513	11	US-11-087-099-7631	Sequence 7631, Ap
43	323.5	19.4	611	11	US-11-087-099-8358	Sequence 8358, Ap
44	322.5	19.3	278	8	US-10-370-959-17	Sequence 17, Appl
45	322.5	19.3	278	8	US-10-370-959-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-10-784-004-373

; Sequence 373, Application US/10784004
; Publication No. US20060084066A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec
; TITLE OF INVENTION: Surrogate Markers of Pain
; FILE REFERENCE: 08201.6029-00000
; CURRENT APPLICATION NUMBER: US/10/784,004
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 1251
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 373
; LENGTH: 455
; TYPE: PRT
; ORGANISM: rat
US-10-784-004-373

  Query Match   67.8%; Score 1131.5; DB 9; Length 455;
  Best Local Similarity   72.5%;
  Matches 214; Conservative 30; Mismatches 44; Indels 7; Gaps 5;

Qy   1 MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSSGFGSVYSGIR 57
              ||||||||||||||| |:|:||| || :|: :|||||||||||||:|||||||||
Db   130 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVVAGSR 188

Qy   58 VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
              :||.||||||||:|:||:|||||||||||||||||:|| |:|||||||||||||||||
Db   189 IADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 247

Qy   116 FVLILERPEPVQDLFDFITTERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLI 175
              |:|:|||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db   248 FLVLERPEPAQDLFDFITTERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV 307

Qy   176 DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
              ||||||||||||||||:|||||||||||||||||||||||||||||||:|||||||||||
Db   308 DLRSGELKLIDFGSGAVLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 367

Qy   236 VCGDIPFEHDEEIVKGQVYFRQVSSECQHLLRWCLSLRPSDRPSFEEIQNHPWM 290
              |||||||||||:|||||||||:|:::|||||||||:||||:|||||||:|||||
Db   368 VCGDIPFEQDEEILRGRLLFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM 422

RESULT 2

US-10-511-937-2982
Sequence 2982, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200010A
; CURRENT APPLICATION NUMBER: 2004-10-19
; CURRENT FILING DATE:
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patentin version 3.2

SEQ ID NO 2982
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2982

Query Match 52.1%; Score 869; DB 8; Length 334;
Best Local Similarity 55.9%; Pred. No. 6.5e-67;
Matches 170; Conservative 43; Mismatches 73; Indels 18; Gaps 3;

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Qy  28 GKEKEPLESQYQVGPLLGSGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP  87
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Db  22 GKDREAFEAEYRLGPLLGKGGFGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP  81

Qy  88 MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR  145
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Db  82 LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR  141

Qy 146 SFFWQVLEAVRHCNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTR  205
        ||| || |:|:| :|:|||||||||||||| |||:|||||||||||:|: |||||||
Db 142 CFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTR  201

Qy 206 VYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFEHDEEIVKGQVYFRQRVSSECQH  265
        ||||||| :|: | :||  |:|||||| ||||||||||| |:||||| :|     :|
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Qy 266 LIRWCLSLRPSDRPSFEEIQNHPWMQ---DVLLPQ-----------ATAEIHLHSLSP  309
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Db 262 LIRRCLAPKPSSRPSLEEILLDPWMQTPAEDVTQPLQRRPCPFGLVLATLSLAWPGLAP  321

Qy 310 SPSK 313
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Db 322 NGQK 325
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RESULT 3
US-10-501-841-32
Sequence 32, Application US/10501841
Publication No. US20060084055A1
GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
; TITLE OF INVENTION: and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058-014402PC
; CURRENT APPLICATION NUMBER: US/10/501,841
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 32
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-841-32

Query Match 52.1%; Score 869; DB 9; Length 334;
Best Local Similarity 55.9%; Pred. No. 6.5e-67;
Matches 170; Conservative 43; Mismatches 73; Indels 18; Gaps 3;

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Qy  28 GKEKEPLESQYQVGPLLGSGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP  87
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Db  22 GKDREAFEAEYRLGPLLGKGGFGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP  81

Qy  88 MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR  145
        :|| ||:|    |:|||||||||:||  |::| |:||| ||||||:|||:| | ||:
Db  82 LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR  141

Qy 146 SFFWQVLEAVRHCNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTR  205
        ||| || |:|:| :|:|||||||||||||| |||:|||||||||||:|: |||||||
Db 142 CFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTR  201

Qy 206 VYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFEHDEEIVKGQVYFRQRVSSECQH  265
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Db 202 VYSPPEWISRHQVHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA  261

Qy 266 LIRWCLSLRPSDRPSFEEIQNHPWMQ---DVLLPQ-----------ATAEIHLHSLSP  309
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Qy 310 SPSK 313
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Db 322 NGQK 325
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RESULT 4
US-10-501-841-40
Sequence 40, Application US/10501841
Publication No. US20060084055A1
GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
; TITLE OF INVENTION: and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058-014402PC
; CURRENT APPLICATION NUMBER: US/10/501,841
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 40

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LENGTH: 311
TYPE: PRT
ORGANISM: Homo sapiens
US-10-501-841-40

Query Match    51.9%;  Score 866.5;  DB 9;  Length 311;
Best Local Similarity   58.0%;  Pred. No. 9.7e-67;
Matches 166;  Conservative  41;  Mismatches  74;  Indels  5;  Gaps  2;

Qy   28  GKEKEPLESQYQVGPLLGSGSGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP  87
         |||| ||:|: || || ||||  :: :: ||| ||| |||||:| ::|| :| |||:| |
Db   22  GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPNRVLGWSPLSDSVTCP  81

Qy   88  MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPPVQDLFDFITERGALQEELAR  145
         :|| || || :  | ||||||||||| :  :|:|||| | |||||:||| | | ::|:
Db   82  LEVALLWKVGAGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR  141

Qy  146  SFFWQVLEAVRHCHNCGVLHRDIKDENILIIDLNRGELKLIDFGSSGALLKDTVYTDFDGTR  205
         .|| ||: |::||| .|| ||||||||| ||| ||  ||||||||||||:| :||||||||
Db  142  CFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSSGALLHDEPYTDFDGTR  201

Qy  206  VYSPPEWIRYHYRHGRSAAVWSLGILLLYDMVCCGDIPFEHDEEIVKGQVYFRQRVSSECQH  265
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Db  202  VYSPPEWISRHQYHALPATVWSLGILLLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA  261

Qy  266  LIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATAEIHLHSLSPSP  311
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Db  262  LIRRCLAPKPSRSRPSLEEILLDPWMQ---TPAEDVPLNPSKGGPAP  304


RESULT 5
US-11-103-065-2
Sequence 2, Application US/11103065
Publication No. US20050281B9A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel E., Lora, Jose M.
TITLE OF INVENTION: 2150, Human Protein Kinase Family
FILE REFERENCE: MP12001-137P1RNM
CURRENT APPLICATION NUMBER: US/11/103,065
CURRENT FILING DATE: 2005-04-11
PRIOR APPLICATION NUMBER: US/10/184,563
PRIOR FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/301,702
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 311
TYPE: PRT
ORGANISM: Homo sapiens
US-11-103-065-2

Query Match    51.9%;  Score 866.5;  DB 11;  Length 311;
Best Local Similarity   58.0%;  Pred. No. 9.7e-67;
Matches 166;  Conservative  41;  Mismatches  74;  Indels  5;  Gaps  2;

Qy   28  GKEKEPLESQYQVGPLLGSGSGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP  87
         |||| ||:|: || || ||||  :: :: ||| ||| |||||:| ::|| :| |||:| |
Db   22  GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPNRVLGWSPLSDSVTCP  81

Qy   88  MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPPVQDLFDFITERGALQEELAR  145
         :|| || || :  | ||||||||||| :  :|:|||| | |||||:||| | | ::|:
Db   82  LEVALLWKVGAGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR  141

Qy  146  SFFWQVLEAVRHCHNCGVLHRDIKDENILIIDLNRGELKLIDFGSSGALLKDTVYTDFDGTR  205
         .|| ||: |::||| .|| ||||||||| ||| ||  ||||||||||||:| :||||||||
Db  142  CFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSSGALLHDEPYTDFDGTR  201

Qy  206  VYSPPEWIRYHYRHGRSAAVWSLGILLLYDMVCCGDIPFEHDEEIVKGQVYFRQRVSSECQH  265
         ||||||| :||: |  | :|||||||||||||| ||||| |:||  ||| :|:| |||  :
Db  202  VYSPPEWISRHQYHALPATVWSLGILLLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA  261

Qy  266  LIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATAEIHLHSLSPSP  311
         |||.|| :.|| ||| ||| : ||||   :: | |||  : :| .|
Db  262  LIRRCLAPKPSRSRPSLEEILLDPWMQ---TPAEDVPLNPSKGGPAP  304
```

```
RESULT 6
US-10-505-928-690
Sequence 690, Application US/10505928
Publication No. US20060085332A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
SEQ ID NO 690
LENGTH: 661
TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-690

Query Match    22.9%;  Score 381.5;  DB 8;  Length 661;
Best Local Similarity   34.8%;  Pred. No. 9e-25;
Matches  93;  Conservative  47;  Mismatches 112;  Indels  15;  Gaps  8;

Qy   31  KEPLESQYQVGPLLGSGSGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEV  90
         |: |..:|  |||| || | :| :|:|:   |  .|||| |:  |    : |:   :|:  :
Db   48  KHNLKHRYELQETLGKGTYGKVKRATERFSGRVVAIKSIRKDKIKDEQDM---VHIRREI  104

Qy   91  VLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQ  150
         :::    |: ||:  ::|:| : |.|:|:|::|: ||  |:::|   | |:: :: .| |
Db  105  EIMS--SLRNPHIISIYEVPENKDKIVIIMEYASK-GELYDYISERRRLSERETHFFRQ  161

Qy  151  VLEAVRHCHNCGVLHRDIKDENILIIDLNRGELKLIDFG--SGALLKDTVYTDFDGTRVYSP  209
         :: || :||.||||||:| ||||| |:  .  | |||||  :  :|| |   || |. :|:|
Db  162  IVSAVHYCHKNGVVHRDLKLENILLDDN-CNIKIADFGLSNLYQKDKFLQTFCGSPLYAS  220

Qy  210  PEWIRYHYRHGRSAAVWSLGILLLYDMVCCGDIP---FEHD---EEIVKGQVYFRQRVSSEC  263
         ||:      |  | : || :|:|| ::|  | ||   |: |   |:|:  | || : :.|
Db  221  PEIVNGRPYRGPEVDSWALGVLLYTLVYGTMPFDGDHKNLIRQISSGE-YREPTQPSDA  279

Qy  264  QHLIRWCLSLRPSDRPSFEEIQNHPWM  290
         : |||| | :.| ||| ||:: :|:|:
Db  280  RGLIRWMLMVNPDRRATIEDIANHWWV  306


RESULT 7
US-10-877-346-74
Sequence 74, Application US/10877346
Publication No. US20060014153A1
GENERAL INFORMATION:
APPLICANT: Gerlach, Valerie L
APPLICANT: Macdougall, John R
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David
APPLICANT: Gunther, Erik
APPLICANT: Ellerman, Karen
APPLICANT: Grosse, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Padigaru, Muralidhara
APPLICANT: Kekuda, Ramesh
APPLICANT: Spytek, Kimberly A
APPLICANT: Leach, Martin D
APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-124
```

CURRENT APPLICATION NUMBER: US/10/877,346
CURRENT FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US/09/964,956
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,808
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,064
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,065
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,135
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/237,434
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/238,321
PRIOR FILING DATE: 2000-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 127
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 74
LENGTH: 256
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Protein kinase
OTHER INFORMATION: domain Consensus Sequence
US-10-877-346-74

Query Match 22.7%; Score 378.5; DB 9; Length 256;
Best Local Similarity 36.2%; Pred. No. 5e-25;
Matches 96; Conservative 49; Mismatches 97; Indels 23; Gaps 9;

```
Qy   38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
           :||  |||||  |||  ||| |  |  |: :: :|: ||
Db    1 YELGEKLGSGAFGKVYKGHKDTGEIVAIKILKKRSLSE----KKKRFLREIQILIRLS 55

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERG-ALQEELARSFFWQVLEAVR 156
           ::|||  |  ||||| : | |  | :|| || :||  |   | : |:| |::
Db   56 --HPNIVRLLGVFEEDHLYLVMEYMEG--GDLFDYLRRNGLLLSEKEAKKIALLQIIRGIE 112

Qy  157 HCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVY---TDFDGTRVYSPPEWI 213
            |  | |:||||:::|||:  ||| |: ::: |||  |:||  |      | |  |:|| |
Db  113 YLHSRGIVHRDLKPENILLDEN-GTVKIADFGLARKLESSSSYEKLTTFVGTPEYMAPEVL 171

Qy  214 RYRYHGRSAAVWSLGILLYDMVCGDIPF----EHDEEIVKGQVYFRQRV------SSECQ 264
           ||  | ||| |||||::||:|  |  :|:    :   |: | ||  |          ::
Db  172 EGRGYSSK-VDVWSLGVILYELLTGKLPPGIDLPELEELFRIKERPRLLPLPPNCSEELK 230

Qy  265 HLIRWCLSLRPSDRPSFEEIQNHPW 289
           |  || |  | ||||:|| | |||:
Db  231 DLIKKCLNKDPEKRPTAKEILNHPW 255
```

RESULT 8
US-11-087-099-9816
Sequence 9816, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 9816
LENGTH: 504
TYPE: PRT
ORGANISM: Cucumis sativus
US-11-087-099-9816

Query Match 22.0%; Score 367; DB 11; Length 504;
Best Local Similarity 34.4%; Pred. No. 1.1e-23;
Matches 90; Conservative 51; Mismatches 105; Indels 16; Gaps 8;

```
Qy   38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
Db    8 YKLGKTLGIGSFGKVKIAEHALTGHKVAIKILNRKIKN---LDMEEKVRREIKILRLFM 64

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
Db   65 --HPHIIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 121

Qy  158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD-TVYTDFD-GTRVYSPPEWIRYH 216
Db  122 CHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 180

Qy  217 RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI------VKGQVY-FRQRVSSECQHLIRW 269
Db  181 LYAGPEVDVDWSCGVILYALLCGTLPFD-DENIPLNLFKKIKGGIYTLPSHLSSGARELIPS 239

Qy  270 CLSLRPSDRPSFEEIQNHPMMQ 291
Db  240 MLVVDPMKRITIPEIRQHPWFQ 261
```

RESULT 9
US-10-501-357
Sequence 357, Application US/10501035
Publication No. US20060046249A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
FILE REFERENCE: D0185 PCT
CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US 60/350,061
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
SOFTWARE: PatentIn version 3.2
SEQ ID NO 357
LENGTH: 950
TYPE: PRT
ORGANISM: Homo sapiens
US-10-501-035-357

Query Match 22.0%; Score 367; DB 9; Length 950;
Best Local Similarity 31.8%; Pred. No. 2.5e-23;
Matches 87; Conservative 52; Mismatches 113; Indels 22; Gaps 7;

```
Qy   38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
Db   44 YDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQL---DAVNLEKIYREVQIMKMLD 99

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
Db  100 --HPHIIKLYQVMETKSMLYLVTEYAKU-GEIFDYLANHGRLNESEAARKFWQLLSAVDY 156

Qy  158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD-TVYTDFDGTRVYSPPEWIRYH 216
Db  157 CHGRKIVHRDLKAENLLLD-NNMNIKIADFGFGNFFKSGELLATWCGSPPYAAPEVFEGQ 215

Qy  217 RYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEIVKGQVYFRQRVSSECQHLIRWC 270
Db  216 QYEGPQLDIWSMGVVLYVLLCGALPFDDGPTLPILRQRVLEGRFRIPYFMSEDCEHLIRRM 275

Qy  271 LSLRPSDRPSFEEIQNHPWM-----QDVLLPQ 297
Db  276 LVLDPSKRLTIAQIKEHKWMLIEVPVQRPVLYPQ 309
```

RESULT 10
US-11-241-056-11
Sequence 11, Application US/11241056
Publication No. US20060248007A1
GENERAL INFORMATION:
;   APPLICANT: Immunex Corporation
;   APPLICANT: Bird, Timothy A.
;   APPLICANT: Virca, G. Duke
;   APPLICANT: Martin, Unja
;   APPLICANT: Anderson, Dirk M.
;   TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
;   FILE REFERENCE: 2923-US
;   CURRENT APPLICATION NUMBER: US/11/241,056
;   CURRENT FILING DATE: 2005-09-30
;   PRIOR APPLICATION NUMBER: US/09/980,464
;   PRIOR FILING DATE: 2001-11-27
;   NUMBER OF SEQ ID NOS: 36
;   SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 11
;   LENGTH: 631
;   TYPE: PRT
;   ORGANISM: Mus musculus

US-11-241-056-11

Query Match   21.9%;   Score 364.5;   DB 11;   Length 631;
Best Local Similarity   32.9%;   Pred. No. 2.4e-23;
Matches 96; Conservative 49; Mismatches 116; Indels 31; Gaps 9;

Qy   22 ANKLAPGKEKEP-----------------------------LESQYQVGPLLGSGGFGFGSVYSGIRVADNLPV 64
                                                      |:| ||||.|:|.|:||:||: :||:
Db   24 ARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTYGKVKKA-RESSGRLV 82

Qy   65 AIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSSGVIRLLDWFERPDSFVLILERPE 124
                |:||| |:|||||| ||| |::|.||||::| |||:||.||:|:|: :||
Db   83 AIKSIRKDKIKDEQDL---LHIRREIEIMS--SLNHHIIAIHEVFENSSKIVIMEYAS 137

Qy   125 PVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRGELKL 184
                ||:|||| :|:|| || :|||||.|| ||:|:|:|||.||||||||.:|| ||.|:||
Db   138 R-GDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDLKLENILLDAN-GNIKI 195

Qy   185 IDFG-SGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFE 243
                |||| .|||||||||.||||||||||||:| |:|: :||:||||||||:||||||.||
Db   196 ADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSLGVLLYILLVHGTMPFD 255

Qy   244 -HDEEIVKGQV----YFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM 290
                  |:|:.|:|| |:|||||||:||:| :|:||:|||:||:|.|:||||
Db   256 GQDHKILVKQISNGAYREPPKEPSDACGLIRWLLMVNPTRRATLEDVASHWWV 307

Qy   270 CLSLRPSDRPSFEEIQNHPWMQ 291
               ||:||:|||:||:|.|:||||:
Db   251 MLIVDPMKRMTIPSIRLHPWFQ 272

RESULT 11
US-11-087-099-11500
Sequence 11500, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
;   APPLICANT: Abad, Mark S. et al.
;   TITLE OF INVENTION: Genes and Uses for Plant Improvement
;   FILE REFERENCE: 38-21(53450)B EP
;   CURRENT APPLICATION NUMBER: US/11/087,099
;   CURRENT FILING DATE: 2005-03-22
;   NUMBER OF SEQ ID NOS: 12464
;
; SEQ ID NO 11500
;   LENGTH: 514
;   TYPE: PRT
;   ORGANISM: Lycopersicon esculentum

US-11-087-099-11500

Query Match   21.5%;   Score 358;   DB 11;   Length 514;
Best Local Similarity   33.2%;   Pred. No. 6.8e-23;
Matches 87; Conservative 54; Mismatches 105; Indels 16; Gaps 8;

Qy   38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97

RESULT 12
US-10-877-346-72
Sequence 72, Application US/10877346
Publication No. US20060141153A1
GENERAL INFORMATION:
;   APPLICANT: Gerlach, Valerie L
;   APPLICANT: MacDougall, John R
;   APPLICANT: Smithson, Glennda
;   APPLICANT: Millet, Isabelle
;   APPLICANT: Stone, David
;   APPLICANT: Gunther, Erik
;   APPLICANT: Ellerman, Karen
;   APPLICANT: Grosse, William M
;   APPLICANT: Alsobrook II, John P
;   APPLICANT: Lepley, Denise M
;   APPLICANT: Burgess, Catherine E
;   APPLICANT: Padigaru, Muralidhara
;   APPLICANT: Kekuda, Ramesh
;   APPLICANT: Spytek, Kimberly A
;   APPLICANT: Leach, Martin D
;   APPLICANT: Shimkets, Richard A
;   TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
;   FILE REFERENCE: 21402-124
;   CURRENT APPLICATION NUMBER: US/10/877,346
;   CURRENT FILING DATE: 2004-06-25
;   PRIOR APPLICATION NUMBER: US/09/964,956
;   PRIOR FILING DATE: 2001-09-26
;   PRIOR APPLICATION NUMBER: 60/235,631
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: 60/235,633
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: 60/235,808
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: 60/236,064
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: 60/236,065
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: 60/236,066
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: 60/236,135
;   PRIOR FILING DATE: 2000-09-28
;   PRIOR APPLICATION NUMBER: 60/237,434
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/238,321
;   PRIOR FILING DATE: 2000-10-05
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 127
;   SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 72
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:

Qy   19 YKLGKTLGIGSFGKVKIAEHTLTGHKVAVKILNRRKIRN---MDMEEKVRREIKILRLFM 75
                |:|| ||| |||::|:|.|| : :|:: || |: :: | |:|:||| :|.|:
Db   19 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 75

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
                :: ::|:|: :: | |:| : : ::|:|:::|| ::| | | : |: ||
Db   76 --HPHIIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEXGRLQODEANFFQQIISGVEY 132

Qy   158 CHNCGVLHRDIKDENILLIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH 216
                || |::|||||||:|| :|:||||||:|||||.||||||||||||| |||||||||:|:
Db   133 CHRNMVVHRDLKPENLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 191

Qy   217 RYHGRSAAVWSLGILLLYDMVCGDIPFEHDEEI------VKGQVY-FRQRVSSECQHLIRW 269
                ||:: || |||| | ||.:| |:|| ::|::: |:||| |.|||||||:||||
Db   192 LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSAGARDLIPR 250

Qy   270 CLSLRPSDRPSFEEIQNHPWMQ 291
               ||:||:|||:||:|.|:||||:
Db   251 MLIVDPMKRMTIPSIRLHPWFQ 272

```
;  OTHER INFORMATION: Description of Artificial Sequence:
;  OTHER INFORMATION: Serine/Threonine protein kinase Consensus
;  OTHER INFORMATION: Sequence
US-10-877-346-72

  Query Match             21.3%;  Score 355.5;  DB 9;  Length 256;
  Best Local Similarity   33.0%;  Pred. No. 4.7e-23;
  Matches   88;  Conservative   56;  Mismatches   96;  Indels   27;  Gaps    8;

Qy    38 YQVGPLLGSGGGFGSVYSGIRVADNLPVAIKHYEKDRISDWGELPNGTRVPMEVVLLKKVS 97
            :|||||||||||||||||||||::|.:|    ||:||::|||::||||:|:||||:||:||
Db     1 YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKEKL----KKKKRERLREIKILKKLD 56

Qy    98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
            ::|:|     |||:||||||||||:|||||:||:|:::|||||:||:||||:||:|:|:
Db    57 --HPNIVKLYDVFEDDDKLYLVMEYCEG--GDLFDLLKKRGRLSEDEARFYARQILSALEY 113

Qy   158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD--TVVTDFDGTRVYSPPEWIRY 215
            |:|:|||||||||||||||||||:|||||||:||||||  :||||||||||:||||||||
Db   114 LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171

Qy   216 HRYHGRSAAVWSLGILILYDMVCGDIPFEHDEIIVKGQVYFRQ----------RVSSE 262
            ||:|||||||||||||:||||||||||||||||||::|:|||          ::|||
Db   172 GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL----ALFKKIGKPPPPFPPPEWKISPE 228

Qy   263 CQHLIRWCLSLRPSDRPSFEEIQNHPW 289
            :||||:||||||||||||||||||||||
Db   229 AKDLIKLLVKDPEKRLTAEEALEHPF 255


RESULT 13
US-11-113-424-183
;  Sequence 183, Application US/11113424
;  Publication No. US20050260713A1
;  GENERAL INFORMATION:
;  APPLICANT: Gangolli et al.
;  TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-225
;  CURRENT APPLICATION NUMBER: US/11/113,424
;  CURRENT FILING DATE: 2005-04-21
;  PRIOR APPLICATION NUMBER: 60/256,704
;  PRIOR FILING DATE: 2000-12-19
;  PRIOR APPLICATION NUMBER: 60/311,590
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/257,314
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: 60/311,613
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/315,617
;  PRIOR FILING DATE: 2001-08-29
;  PRIOR APPLICATION NUMBER: 60/307,506
;  PRIOR FILING DATE: 2001-07-24
;  PRIOR APPLICATION NUMBER: 60/322,358
;  PRIOR FILING DATE: 2001-09-14
;  PRIOR APPLICATION NUMBER: 60/294,075
;  PRIOR FILING DATE: 2001-05-29
;  PRIOR APPLICATION NUMBER: 60/288,153
;  PRIOR FILING DATE: 2001-05-02
;  NUMBER OF SEQ ID NOS: 190
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 183
;  LENGTH: 256
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: consensus
;  OTHER INFORMATION: sequence
US-11-113-424-183

  Query Match             21.3%;  Score 355.5;  DB 11;  Length 256;
  Best Local Similarity   33.0%;  Pred. No. 4.7e-23;
  Matches   88;  Conservative   56;  Mismatches   96;  Indels   27;  Gaps    8;
```

```
Qy    38 YQVGPLLGSGGGFGSVYSGIRVADNLPVAIKHYEKDRISDWGELPNGTRVPMEVVLLKKVS 97
            :|||||||||||||||||||||::|.:|    ||:||::|||::||||:|:||||:||:||
Db     1 YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKEKL----KKKKRERLREIKILKKLD 56

Qy    98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
            ::|:|     |||:||||||||||:|||||:||:|:::|||||:||:||||:||:|:|:
Db    57 --HPNIVKLYDVFEDDDKLYLVMEYCEG--GDLFDLLKKRGRLSEDEARFYARQILSALEY 113

Qy   158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD--TVVTDFDGTRVYSPPEWIRY 215
            |:|:|||||||||||||||||||:|||||||:||||||  :||||||||||:||||||||
Db   114 LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171

Qy   216 HRYHGRSAAVWSLGILILYDMVCGDIPFEHDEIIVKGQVYFRQ----------RVSSE 262
            ||:|||||||||||||:||||||||||||||||||::|:|||          ::|||
Db   172 GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL----ALFKKIGKPPPPFPPPEWKISPE 228

Qy   263 CQHLIRWCLSLRPSDRPSFEEIQNHPW 289
            :||||:||||||||||||||||||||||
Db   229 AKDLIKLLVKDPEKRLTAEEALEHPF 255


RESULT 14
US-11-087-099-12331
;  Sequence 12331, Application US/11087099
;  Publication No. US20060419961A1
;  GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE: 2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
;  SEQ ID NO 12331
;  LENGTH: 504
;  TYPE: PRT
;  ORGANISM: Solanum tuberosum
US-11-087-099-12331

  Query Match             21.0%;  Score 350.5;  DB 11;  Length 504;
  Best Local Similarity   32.5%;  Pred. No. 2.9e-22;
  Matches   98;  Conservative   53;  Mismatches  112;  Indels   39;  Gaps   12;

Qy    28 GKEKEPLESQYQVGPLLGSGGGFGSVYSGIRVADNL----PVAIKHVEKDRISDWGELPNG 83
            |:  |:|||:|||||||||||||||||||||||||      |:|||:::|||:|||||||
Db     7 GIAESPYLRNYRVGKTLGHGSFGKV---------------KIAEHLLGHKVAIKILNRRKM- 53

Qy    84 TRVP-MEVVLLKKVS----SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGA 138
            ||     |||:||||     ||:|| ||||||||||||||:|:|||||:||:|:|:|||
Db    54 -KTPDMEEKLRREIKICRLFVHPHVIRLYEVIETPTDIYVVMEYVKS-GELFDYIVEKGR 111

Qy   139 LQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVY 198
            |:|||||:||||:|||:|:|::|||:||||||||||||||||:||||||||:|||:||:|
Db   112 LQEDEARKIFQQIIAGVEYCHKNMVVHRDLKPENLLLDARR-NVKIADFGLGNIMRDGHF 170

Qy   199 TDFD-GTRVYSPPEWIRYHRYHGRSAAVWSLGILILYDMVCGDIPFEHDEEI-----VKG 251
            ||   |||||||||||||:|:||||||||||||||||||||||||||||||     ||
Db   171 LKTSCGSPNYAAPEVVSGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKS 229

Qy   252 QVY-FRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVL-----LPQATAEIHLH 305
            |:|  |:|:|::||||||||||||||||||||||||||||:|:|     ||::|:|:|||
Db   230 GVVTLPSHLSPLARDLIPRMLIVDPMKRISVPDIRQHQWFKIHLPRYLAVPPPDARQHLK 289

Qy   306 SL 307
            ||
Db   290 KL 291
```

```
RESULT 15
US-11-087-099-3997
;  Sequence 3997, Application US/11087099
;  Publication No. US20060419961A1
;  GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
```

```
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
;  SEQ ID NO 3997
;  LENGTH: 512
;  TYPE: PRT
;  ORGANISM: Solanum tuberosum
US-11-087-099-3997

  Query Match         21.0%;  Score 350;  DB 11;  Length 512;
  Best Local Similarity   31.7%;  Pred. No. 3.3e-22;
  Matches   84;  Conservative   60;  Mismatches   99;  Indels   22;  Gaps   8;

Qy     38 YQVGPLLGSSGGGFGSSVYSGIRVADNL----PVAIKHVEKDRISDWGELPNGTRVPMEVVLL 93
          |::|     |:|::  |:    ||:  |       :|:||  : |:   || ||  || |:|
Db     19 YKLGKTLGIGSFGKV----KIAHTLIGHKVAVKILNRRKIRN---MDMEEKVSREIKIL 71

Qy     94 KKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLE 153
          ||  :: |  |: | ||: |: | ::|| : :|||:: |::  |  :|: :|| ||: |
Db     72 RLFMHGH--ISRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIIS 128

Qy    154 AVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEW 212
          |: || | |||||||:|||| | |: || |||||:   | |||::  : ||| || ||
Db    129 GVEYCHINMVVHRDLKPENLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEV 187

Qy    213 IRYHRYHGRSAAVWSLGILLLYDMVCGDIPFEHD------EEIVKGQYYFRQRVSSECQHL 266
          |||  || | |||:|||::|||:||  ||| ||         |:||||:||: ::   |
Db    188 ISGKLYAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFKKIKGGYITLPSHLSAGARDL 247

Qy    267 IRWCLSLRPSDRPSFEEIQNHPWMQ 291
          |  || | | ||||::|| ||| ||
Db    248 IPRMLIVDPMKRMTIPEIRLHPWFQ 272

Search completed: May 4, 2006, 05:32:58
Job time : 16.3333 secs
```

OM protein - protein search, using sw model

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GenCore version 5.1.7

Run on: May 4, 2006, 05:12:40 ; Search time 113.667 Seconds
                                      (without alignments)
                                      1209.902 Million cell updates/sec

Title: US-10-705-757-4
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRAAPCNDL.........LLPQATAEIHLHSLSPPSK 313
Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Post-processing: Minimum Match 0%
                 Maximum Match 100%
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :   A_Geneseq_21:*
               Listing first 45 summaries

               1: geneseqp1908s:*
               2: geneseqp1990s:*
               3: geneseqp2000s:*
               4: geneseqp2001s:*
               5: geneseqp2002s:*
               6: geneseqp2003as:*
               7: geneseqp2003bs:*
               8: geneseqp2004s:*
               9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	ID	Description
1	1668	100.0	313	5	ABG33016	Abg33016	Rat prote
2	1668	100.0	313	6	AAO19789	Aao19789	Rat PIM1
3	1668	100.0	313	6	ABR62938	Abr62938	Rat serin
4	1668	100.0	313	9	AEB96039	Aeb96039	Norway ra
5	1636	98.1	313	5	ABP54943	Abp54943	Human Pim
6	1636	98.1	313	6	ABG33017	Abg33017	Human pro
7	1636	98.1	313	6	AAO19788	Aao19788	Human PIM
8	1636	98.1	313	7	ABU61613	Abu61613	Human PIM
9	1636	98.1	313	7	ABR62939	Abr62939	Human ser
10	1636	98.1	313	7	ADE55368	Ade55368	Human Pro
11	1636	98.1	313	7	ADF45083	Adf45083	Human kin
12	1636	98.1	313	8	ADO19690	Ado19690	Human PRO
13	1636	98.1	313	8	ADR88370	Adr88370	Human PIM
14	1636	98.1	313	8	ADP24227	Adp24227	PRO polyp
15	1636	98.1	313	8	ADT07365	Adt07365	Human pro
16	1636	98.1	313	8	ADT14636	Adt14636	Human pro
17	1636	98.1	313	8	ADY86782	Ady86782	Human Pim
18	1636	98.1	313	9	AEA89424	Aea89424	Human Pim
19	1636	98.1	313	9	AEB96037	Aeb96037	Human PIM
20	1623	97.3	313	2	AAW08139	Aaw08139	Human cyt
21	1623	97.3	313	3	AAY87959	Aay87959	Human CR7
22	1623	97.3	313	3	ADI57202	Adi57202	Human PIM
23	1623	97.3	313	8	ADN03170	Adn03170	Human PIM
24	1623	97.3	313	9	ADY85580	Ady85580	Catalytic
25	1584	95.0	313	5	ABG33015	Abg33015	Mouse pro
26	1584	95.0	313	6	AAO19790	Aao19790	Murine PI
27	1584	95.0	313	7	ABR62940	Abr62940	Mouse ser
28	1584	95.0	313	8	ADN97347	Adn97347	Murine Pi
29	1584	95.0	313	9	ADR88371	Adr88371	Mus muscu
30	1584	95.0	313	9	AEA19261	Aea19261	Mouse Pim
31	1578	94.6	313	9	AEB96041	Aeb96041	House mou
32	1345	80.6	253	8	AEA19263	Aea19263	Mouse Pim
33	1345	80.6	253	8	ADI57241	Adi57241	PIM1 domi
34	1304.5	78.2	257	2	AAY43942	Aay43942	Rat prote
35	1267.5	76.0	254	8	ADK71853	Adk71853	Human kin
36	1229	73.7	233	8	ADT07367	Adt07367	Human pro
37	1137	68.2	323	8	ADR88376	Adr88376	Columnix
38	1137	68.2	323	8	AAY06886	Aay06886	HWHHJ20 p
39	1137	68.2	374	8	ADX91611	Adx91611	Plant ful
40	1135	68.0	326	4	AAB29788	Aab29788	Human ser
41	1135	68.0	326	5	AAE23834	Aae23834	Human HKI
42	1135	68.0	326	5	ABG33011	Abg33011	Human ser
43	1135	68.0	326	7	ABR62932	Abr62932	Human cal
44	1135	68.0	326	8	ADJ96625	Adj96625	Human pro
45	1135	68.0	326	8	ADL97960	Adl97960	Human PIM

ALIGNMENTS

RESULT 1
ID   ABG33016 standard; protein; 313 AA.
XX
AC   ABG33016;
XX
DT   20-DEC-2002 (first entry)
XX
DE   Rat protein kinase phosphorylation site #2.
XX
KW   HKID-1; serine/threonine kinase; cellular proliferative disorder;
KW   differentiative disorder; cancer; haematopoietic neoplastic disorder;
KW   Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML;
KW   Waldenstrom's macroglobulinaemia; WM; rat.
OS   Rattus norvegicus.
XX
PN   US2002115120-A1.
XX
PD   22-AUG-2002.
XX
PF   04-OCT-2001; 2001US-00971791.
XX
PR   26-JAN-1999; 99US-00237543.
PR   23-AUG-2000; 2000US-00644450.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
XX
DR   WPI; 2002-712471/77.
XX
PT   Modulating levels or activity of HKID-1 polypeptides, a member of
PT   serine/threonine kinase superfamily, for treating cancer, by contacting
PT   cell expressing the polypeptide with a modulator of the polypeptide.
XX
PS   Example 3; Page 39-40; 48pp; English.
XX
CC   The invention describes a method of modulating the level or activity of
CC   human HKID-1 polypeptide, a member of serine/threonine kinase
CC   superfamily. The method involves contacting a cell expressing the
CC   polypeptide or nucleic acid with an agent to modulate the level or
CC   activity of polypeptide, or level of nucleic acid molecule. The method is
CC   useful for modulating the level or activity of HKID-1 polypeptide or
CC   polynucleotide in a subject having or predisposed to having a disorder
CC   involving cancer. Modulating HKID-1 expression or activity is useful for
CC   therapeutic purposes, for treating cellular proliferative and/or

CC   differentiative disorders including cancer or haematopoietic neoplastic
CC   disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
CC   leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
CC   amino acid sequence of a rat protein kinase phosphorylation site
XX
SQ   Sequence 313 AA;

Query Match   100.0%; Score 1668; DB 5; Length 313;
Best Local Similarity   100.0%;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
                        Pred. No. 9.6e-159;

```
Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPSPSK 313
          |||||||||||||
Db  301 EIHLHSLSPSPSK 313
```

RESULT 2
ID   AAO19789 standard; protein; 313 AA.
XX
AC   AAO19789;
XX
DT   11-AUG-2003   (first entry)
XX
DE   Rat PIM1 kinase.
XX
KW   Rat; PIM1 kinase; PIM3 kinase; pain; analgesic.
OS   Rattus sp.
XX
PN   WO2002093173-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-EP005234.
PR   11-MAY-2001; 2001DE-0102305S.
XX
PA   (CHEF) GRUENENTHAL GMBH.
XX
PI   Weihe E, Schaefer MK;
XX
DR   WPI; 2003-120715/11.
DR   N-PSDB; AB269187.
XX
PT   Method for identifying analgesics, useful particularly for treating
PT   chronic pain, by screening compounds for interaction with PIM-1 or -3
PT   kinase, or related compounds.
PS   Claim 1; Fig 1D; 97pp; German.
CC   The present invention relates to a method of identifying pain-regulating
CC   compounds, involving screening candidate compounds for interaction with

CC   PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC   useful for treating chronic pain, particularly of neuropathic or
CC   inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC   neurodegenerative diseases). The present sequence is rat PIM1 kinase
XX
SQ   Sequence 313 AA;

Query Match   100.0%; Score 1668; DB 5; Length 313;
Best Local Similarity   100.0%;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
                        Pred. No. 9.6e-159;

```
Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPSPSK 313
          |||||||||||||
Db  301 EIHLHSLSPSPSK 313
```

RESULT 3
ID   ABR62938 standard; protein; 313 AA.
XX
AC   ABR62938;
XX
DT   04-DEC-2003   (first entry)
XX
DE   Rat serine/threonine protein kinase PIM-1.
XX
KW   Rat; PIM-1; protein kinase; enzyme.
OS   Rattus norvegicus.
XX
PN   WO2003060130-A2.
XX
PD   24-JUL-2003.
XX
PF   20-JAN-2003; 2003WO-EP000492.
PR   19-JAN-2002; 2002EP-00001401.
XX
PA   (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI   Korn M, Mueller G, Schneider R, Tschank G;
XX
DR   WPI; 2003-598536/56.
XX
PT   New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
PT   agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT   treating insulin resistance or type 2 diabetes mellitus.
PS   Example 2; Page 39; 40pp; English.
CC   The present sequence is the protein sequence of the rat serine/threonine
CC   protein kinase and proto-oncogene, PIM-1. PIM-1 proteins are the
CC   paralogues of novel human and murine PIM-3 proteins (see ABR62932 and

SQ   Sequence 313 AA;

Query Match   100.0%; Score 1668; DB 6; Length 313;
Best Local Similarity   100.0%;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
                        Pred. No. 9.6e-159;

```
Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPSPSK 313
          |||||||||||||
Db  301 EIHLHSLSPSPSK 313
```

```
CC  ABR62933) of the invention, which are therefore expected to be involved
CC  in cancer and cell growth regulation. PIM-3 is also involved in the
CC  development of insulin resistance and type 2 diabetes mellitus. The
CC  invention relates to the use of PIM-3 nucleic acids and proteins in:
CC  screening assays for compounds that modulate insulin resistance or type 2
CC  diabetes mellitus; detection assays for detecting insulin resistance or
CC  type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
CC  forensic biology); predictive medicine (e.g. diagnostic or prognostic
CC  assays, monitoring clinical trials, pharmacogenomics); and for
CC  preparing a medicament for the treatment of insulin resistance or type 2
CC  diabetes mellitus
XX
SQ  Sequence 313 AA;

Qy  Query Match             100.0%;  Score 1668;  DB 7;  Length 313;
    Best Local Similarity   100.0%;  Pred. No. 9.6e-159;
    Matches 313;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60

Qy       61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy      121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy      181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy      241  PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy      301  EIHLHSLSPSPSK 313
             |||||||||||||
Db      301  EIHLHSLSPSPSK 313
```

```
RESULT 4
AEB96039
ID   AEB96039 standard; protein; 313 AA.
XX
AC   AEB96039;
XX
DT   20-OCT-2005  (first entry)
XX
DE   Norway rat PIM-1 serine-threonine kinase protein.
XX
KW   micturition disorder; urinary dysfunction; uropathic; gene therapy;
KW   PIM-1 protein kinase; serine-threonine kinase; enzyme.
XX
OS   Rattus norvegicus.
XX
PN   DE102004004894-A1.
XX
PD   18-AUG-2005.
XX
PF   30-JAN-2004; 2004DE-10004894.
XX
PR   30-JAN-2004; 2004DE-10004894.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
PI   Christoph T;
XX
DR   WPI; 2005-556609/57.
DR   N-PSDB; AEB96038.
DR   REFSEQ; NP_058730.
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XX
PT   Identifying substances that regulate PIM kinases, useful for treatment
PT   and diagnosis of urinary incontinence and the urge to urinate, and
PT   similar use of PIM proteins or nucleic acids.
XX
PS   Claim 1; Fig 1D; 37pp; German.
XX
CC   The invention relates to a novel method for identifying substances that
CC   regulate urinary incontinence and the urge to urinate. The method
CC   comprises incubating a test compound with a cell and/or cell preparation
CC   that has synthesized a specific protein of the PIM (proviral integration
CC   site) kinase family and measuring either binding of the test compound to
CC   the PIM kinase, or a functional parameter that is altered by the binding.
CC   The method of the invention demonstrates uropathic and gene therapy
CC   applications and may be useful for treatment and diagnosis of urinary
CC   incontinence and the urge to urinate. The current sequence is that of the
CC   the activity or expression of PIM kinases that are involved in bladder
CC   control. The current sequence is that of the Norway rat PIM-1 serine-
CC   threonine kinase protein of the invention.
XX
SQ   Sequence 313 AA;

Qy   Query Match             100.0%;  Score 1668;  DB 9;  Length 313;
     Best Local Similarity   100.0%;  Pred. No. 9.6e-159;
     Matches 313;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60

Qy       61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy      121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy      181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy      241  PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy      301  EIHLHSLSPSPSK 313
             |||||||||||||
Db      301  EIHLHSLSPSPSK 313
```

```
RESULT 5
ABP54943
ID   ABP54943 standard; protein; 313 AA.
XX
AC   ABP54943;
XX
DT   13-JAN-2003  (first entry)
XX
DE   Human Pim1.
XX
KW   Pim1; tyrosine threonine kinase; TTK; protein kinase; enzyme;
KW   mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
KW   human; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200268444-A1.
XX
PD   06-SEP-2002.
XX
PF   21-FEB-2002; 2002WO-US005278.
XX
```

```
PR   21-FEB-2001; 2001US-0271254P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Reinhard C, Jefferson AB, Chan VW;
XX
DR   WPI; 2002-698650/75.
DR   N-PSDB; ABV73989.
XX
PS   Disclosure; Page 80-81; 113pp; English.
XX
PT   Reducing growth of cancer cells comprises reducing Tyrosine Threonine
PT   kinase (TTK) activity, useful in diagnosing and treating disorders with
PT   abnormal expression levels and activity of TTK, such as lung, colon,
PT   prostate and ovarian cancer.
XX
CC   The present sequence is the protein sequence of human Pim1, a protein
CC   related to tyrosine threonine kinase (TTK, see ABP54938). TTK
CC   polynucleotides and polypeptides of the invention encompass
CC   polynucleotides and polypeptides having sequence similarity or sequence
CC   identity to human TTK and other genes and gene products related to TTK,
CC   such as Pim1. The invention is based on the finding that TTK is
CC   differentially expressed in various forms of cancer. It provides methods
CC   for the identification of cancerous cells, especially breast cancer and
CC   colon cancer cells, by detection of expression levels of TTK, as well as
CC   diagnostic, prognostic and therapeutic methods. These methods can be used
CC   as the basis of rational therapy. Assays for identifying molecules that
CC   modulate the activity of these genes in cancers, as well as methods of
CC   inhibiting tumour growth by inhibiting the activity of TTK are also
CC   provided.
XX
SQ   Sequence 313 AA;

Query Match             98.1%;  Score 1636;  DB 5;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 1.6e-155;
Matches  304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy    1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60
         ||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||:|
Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG  180

Qy  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300
         |||||||:::||||:|||||||||||||||||:|||||||:||||||||||||||||:||
Db  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301  EIHLHSLSPSPSK  313
         |||||||||:|||
Db  301  EIHLHSLSPGPSK  313


RESULT 6
ABG33017
ID   ABG33017 standard; protein; 313 AA.
XX
AC   ABG33017;
XX
DT   20-DEC-2002  (first entry)
XX
DE   Human protein kinase phosphorylation site.
XX
KW   HKID-1; serine/threonine kinase; cellular proliferative disorder;
KW   differentiative disorder; cancer; haematopoietic neoplastic disorder;
KW   Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML;
KW   Waldenstrom's macroglobulinaemia; WM; human.
XX
OS   Homo sapiens.
XX
PN   US2002115120-A1.
XX
PD   22-AUG-2002.
XX
PF   04-OCT-2001; 2001US-00971791.
XX
PR   26-JAN-1999;  99US-00237543.
PR   23-AUG-2000; 2000US-00644450.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
XX
DR   WPI; 2002-712471/77.
XX
PS   Example 3; Page 40-41; 48pp; English.
XX
PT   Modulating levels or activity of HKID-1 polypeptides, a member of
PT   serine/threonine kinase superfamily, for treating cancer, by contacting
PT   cell expressing the polypeptide with a modulator of the polypeptide.
XX
CC   The invention describes a method of modulating the level or activity of
CC   human HKID-1 polypeptide, a member of serine/threonine kinase
CC   superfamily. The method involves contacting a cell expressing the
CC   polypeptide or nucleic acid with an agent to modulate the level or
CC   activity of polypeptide, or level of nucleic acid molecule. The method is
CC   useful for modulating the level or activity of HKID-1 polypeptide or
CC   polynucleotide in a subject having or predisposed to having a disorder
CC   involving cancer. Modulating HKID-1 expression or activity is useful for
CC   therapeutic purposes, for treating cellular proliferative and/or
CC   differentiative disorders including cancer or haematopoietic neoplastic
CC   disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
CC   leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
CC   amino acid sequence of a human protein kinase phosphorylation site
XX
SQ   Sequence 313 AA;

Query Match             98.1%;  Score 1636;  DB 5;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 1.6e-155;
Matches  304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy    1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60
         ||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||:|
Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG  180

Qy  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300
         |||||||:::||||:|||||||||||||||||:|||||||:||||||||||||||||:||
Db  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301  EIHLHSLSPSPSK  313
         |||||||||:|||
Db  301  EIHLHSLSPGPSK  313


RESULT 7
```

AA019788
ID   AA019788 standard; protein; 313 AA.
XX
AC   AA019788;
XX
DT   11-AUG-2003 (first entry)
XX
DE   Human PIM1 kinase.
XX
KW   Human; PIM1 kinase; PIM3 kinase; pain; analgesic.
XX
OS   Homo sapiens.
XX
PN   WO20029173-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-EP005234.
XX
PR   11-MAY-2001; 2001DE-0103055.
XX
PA   (CHEF) GRUENENTHAL GMBH.
XX
PI   Weihe E, Schaefer MK;
XX
DR   WPI; 2003-120715/11.
DR   N-PSDB; AB269186.
XX
PT   Method for identifying analgesics, useful particularly for treating
PT   chronic pain, by screening compounds for interaction with PIM-1 or -3
PT   kinase, or related compounds.
XX
PS   Claim 1; Fig 1B; 97pp; German.
XX
CC   The present invention relates to a method of identifying pain-regulating
CC   compounds, involving screening candidate compounds for interaction with
CC   PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC   useful for treating chronic pain, particularly of neuropathic or
CC   inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC   neurodegenerative diseases). The present sequence is human PIM1 kinase
SQ   Sequence 313 AA;

Query Match   98.1%; Score 1636; DB 6; Length 313;
Best Local Similarity   97.1%; Pred. No. 1.6e-155;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPSPSK 313
              |||||||||||||
Db   301 EIHLHSLSPSPSK 313

RESULT 8

ABU61613
ID   ABU61613 standard; protein; 313 AA.
XX
AC   ABU61613;
XX
DT   11-AUG-2003 (first entry)
XX
DE   Human PIM1 protein.
XX
KW   Human; tyrosine threonine kinase; TTK; cancer; cytostatic;
KW   mitotic checkpoint gene; PIM1.
XX
OS   Homo sapiens.
XX
PN   US2003045491-A1.
XX
PD   06-MAR-2003.
XX
PF   21-FEB-2002; 2002US-00081119.
XX
PR   23-FEB-2001; 2001US-0289813P.
XX
PA   (REIN/) REINHARD C.
PA   (JEFF/) JEFFERSON A B.
PA   (CHAN/) CHAN V W.
XX
PI   Reinhard C, Jefferson AB, Chan VW;
XX
DR   WPI; 2003-456566/43.
DR   N-PSDB; ACA62265.
XX
PT   Detecting cancer in a subject, by comparing expression levels of tyrosine
PT   threonine kinase polypeptide or polynucleotide in a subject cell and a
PT   normal cell, where an increase in the expression level in the test cell
PT   is indicative of cancer.
XX
PS   Disclosure; Page 34-35; 79pp; English.
XX
CC   The invention relates to detecting cancer (other than ovarian cancer) in
CC   a subject, comprising comparing the expression levels of tyrosine
CC   threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or
CC   polynucleotide in a test cell obtained from the subject and in a normal
CC   non-cancer cell, where an increase in the expression level of TTK protein
CC   or nucleic acid in the test cell compared to that in the normal cell,
CC   indicates the presence of cancer other than ovarian cancer. Also included
CC   are reducing growth of a cancerous cell (by contacting a cancerous cell
CC   with an amount of an agent effective to reduce TTK polypeptide activity
CC   in the cell), an assay for identifying a candidate agent that reduces
CC   growth of a cancerous cell (comprising: (i) detecting the activity of a
CC   TTK polypeptide in the presence of a candidate agent; and (ii) comparing
CC   the activity of TTK polypeptide in the presence of a candidate agent
CC   relative to TTK polypeptide activity in the absence of the candidate
CC   agent), identifying an agent that reduces TTK activity (comprising: (i)
CC   contacting a cancerous cell displaying elevated expression of a TTK-
CC   encoding polynucleotide with a candidate agent; and (ii) determining the
CC   effect of the candidate agent on TTK polypeptide activity) and assessing
CC   the prognosis of a cancerous disease other than ovarian cancer in a
CC   subject (comprising: (i) detecting expression of TTK -encoding
CC   polynucleotide in a test cancer cell of a subject; and (ii) comparing a
CC   level of expression of TTK-encoding polynucleotide in the test cancer
CC   cell with a level of expression of the polynucleotide in a control non-
CC   cancer cell, where the level of expression of TTK in the test cancer cell
CC   relative to the level of expression in the control non-cancer cell is
CC   indicative of the prognosis of the cancerous disease). The methods are
CC   useful for detecting cancer (other than ovarian cancer) in a subject,
CC   reducing growth of cancerous cells, identifying a candidate agent that
CC   reduces growth of a cancerous cell, identifying an agent that reduces TTK
CC   activity and assessing the prognosis of a cancerous disease other than
CC   ovarian cancer. The methods are also useful for determining the ability
CC   of a subject to respond to a particular therapy e.g. as a basis of
CC   rational therapy. The present sequence represents a closely related
CC   protein to human TTK, in this case human PIM1 (not defined)
XX

SQ   Sequence 313 AA;

Query Match   98.1%; Score 1636; DB 7; Length 313;
Best Local Similarity   97.1%; Pred. No. 1.6e-155;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
          |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
          ||||||||||| |||
Db   301 EIHLHSLSPGPSK 313

RESULT 9
ID   ABR62939
AC   ABR62939;
XX
DT   04-DEC-2003 (first entry)
XX
DE   Human serine/threonine protein kinase PIM-1.
XX
KW   Human; PIM-1; protein kinase; enzyme.
XX
OS   Homo sapiens.
XX
PN   WO2003060130-A2.
XX
PD   24-JUL-2003.
XX
PF   20-JAN-2003; 2003WO-EP000492.
XX
PR   19-JAN-2002; 2002EP-00001401.
XX
PA   (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI   Korn M, Mueller G, Schneider R, Tschank G;
XX
DR   WPI; 2003-598536/56.
XX
PT   New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
PT   agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT   treating insulin resistance or type 2 diabetes mellitus.
XX
PS   Example 2; Page 40; 40pp; English.
XX
CC   The present sequence is the protein sequence of the human
CC   serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins
CC   are the paralogues of novel human and murine PIM-3 proteins (see ABR62932
CC   and ABR62933) of the invention, which are therefore expected to be
CC   involved in cancer and cell growth regulation. PIM-3 is also involved in
CC   the development of insulin resistance and type 2 diabetes mellitus. The
CC   invention relates to the use of PIM-3 nucleic acids and proteins in:
CC   screening assays for compounds that modulate insulin resistance or type 2

CC   diabetes mellitus; detection assays for detecting insulin resistance or
CC   type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
CC   forensic biology); predictive medicine (e.g. diagnostic or prognostic
CC   assays, monitoring clinical trials, pharmacogenomics); and for
CC   preparing a medicament for the treatment of insulin resistance or type 2
CC   diabetes mellitus

SQ   Sequence 313 AA;

Query Match   98.1%; Score 1636; DB 7; Length 313;
Best Local Similarity   97.1%; Pred. No. 1.6e-155;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
          |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
          ||||||||||| |||
Db   301 EIHLHSLSPGPSK 313

RESULT 10
ID   ADE55368
AC   ADE55368;
XX
DT   29-JAN-2004 (first entry)
XX
DE   Human Protein AAA60089, SEQ ID NO 1183.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
XX
PI   Woolf C, D'urso D, Befort K, Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; AAA60089.
XX
PT   New composition comprising two or more isolated polypeptides, useful for

PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are the vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic construction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 313 AA;

Query Match   98.1%; Score 1636; DB 7; Length 313;
Best Local Similarity   97.1%; Pred. No. 1.6e-155;
Matches   304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGGFGSVSYSGIRVAD 60
         |||||||||||||| ||||||||| |||||||||||||||||||||||||||||| |||| :|
Db   1 MLLSKINSLAHLRRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQETA 300
         |||||||: ||:| |||||||||||||||||| |||||| ||||||||||||||||||||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPSPSK 313
         |||||||| ||||
Db 301 EIHLHSLSPGPSK 313

RESULT 11
ID   ADF45083
AC   ADF45083;
XX
DT   12-FEB-2004 (first entry)
XX
DE   Human kinase PIM1.
XX

KW   Human; protein kinase; enzyme; inhibitor; PIM1.
XX
OS   Homo sapiens.
XX
PN   WO200308121O-A2.
XX
PD   02-OCT-2003.
XX
PF   20-MAR-2003; 2003WO-US008725.
XX
PR   21-MAR-2002; 2002US-03668929P.
XX
PA   (SUNE-) SUNESIS PHARM INC.
XX
PI   Prescott JC, Braisted A;
XX
DR   WPI; 2003-865136/80.
XX
PT   Identifying ligand binding to inactive conformation of target protein
PT   kinase (T) comprises contacting the conformation modified (T) which
PT   contains reactive group at binding site, with ligands and detecting
PT   kinase-ligand conjugate formation.
XX
PS   Disclosure; SEQ ID NO 52; 260pp; English.
XX
CC   The present invention relates to a method for identifying a ligand (L),
CC   which binds to an inactive conformation of target protein kinase (T). The
CC   method involves contacting inactive conformation of target protein (T),
CC   or is modified to contain a reactive group at or near a binding site of
CC   interest, with one or more ligand candidates capable of covalently
CC   bonding to the reactive group thus forming a kinase-(T) conjugate (C).
CC   The method is useful for identifying protein kinase inhibitors that
CC   preferentially bind to inactive conformation of a target protein kinase.
CC   The present sequence is a protein kinase which may be modified via an
CC   amino acid substitution, for use in the method of the invention.
XX
SQ   Sequence 313 AA;

Query Match   98.1%; Score 1636; DB 7; Length 313;
Best Local Similarity   97.1%; Pred. No. 1.6e-155;
Matches   304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGGFGSVSYSGIRVAD 60
         |||||||||||||| ||||||||| |||||||||||||||||||||||||||||| |||| :|
Db   1 MLLSKINSLAHLRRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQETA 300
         |||||||: ||:| |||||||||||||||||| |||||| ||||||||||||||||||||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPSPSK 313
         |||||||| ||||
Db 301 EIHLHSLSPGPSK 313

RESULT 12
ID   AD019690
AC   AD019690;
XX

DT   12-AUG-2004 (first entry)
XX
DE   Human PRO polypeptide #308.
XX
KW   Human; PRO; immune related disorder; systemic lupus erythematosus;
KW   rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW   systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW   autoimmune haemolytic anaemia; autoimmune thrombocytopenia;
KW   diabetes mellitus; renal disease; demyelinating disease;
KW   central nervous system; peripheral nervous system;
KW   demyelinating polyneuropathy; Guillain-Barre syndrome;
KW   chronic inflammatory demyelinating polyneuropathy.
XX
OS   Homo sapiens.
XX
XX
PN   WO200404361-A2.
XX
PD   27-MAY-2004.
XX
PF   06-NOV-2003; 2003WO-US035268.
XX
PR   08-NOV-2002; 2002US-0425235P.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI   Wood WI, Wu TD;
XX
DR   WPI; 2004-420067/39.
DR   N-PSDB; AD019689.
XX
PT   Novel PRO polypeptide e.g. PRO69614, PRO71106, or PRO86388 useful for
PT   treating an immune related disorder such as systemic lupus erythematosus,
PT   rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT   spondyloarthropathy.
XX
PS   Claim 7; SEQ ID NO 616; 1731pp; English.
XX
CC   The invention relates to human PRO polypeptides and the polynucleotides
CC   encoding them. The polypeptides and polynucleotides are useful for
CC   treating and diagnosing immune related disorders in mammals. The immune
CC   related disorders include systemic lupus erythematosus, rheumatoid
CC   arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC   sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC   haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC   mellitus, immune-mediated renal disease, demyelinating diseases of the
CC   central or peripheral nervous system, demyelinating polyneuropathy,
CC   Guillain-Barre syndrome and chronic inflammatory demyelinating
CC   polyneuropathy. This sequence represents a human PRO polypeptide of the
CC   invention.
XX
SQ   Sequence 313 AA;

Query Match   98.1%; Score 1636; DB 8; Length 313;
Best Local Similarity   97.1%;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSEECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
               |||||||||:.:||||||||||||||||||||||||:.|||||||||||||||||||||||
Db   241 PFEHDEEIRGQVFRQRVSSEECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPSPSK 313
               |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 13
ADR88370
ID   ADR88370 standard; protein; 313 AA.
XX
AC   ADR88370;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Human PIM 1 protein.
XX
KW   Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW   G-protein coupled receptor; methyl transferase; ligase; PIM; human.
XX
OS   Homo sapiens.
XX
PN   US2004171062-A1.
XX
PD   02-SEP-2004.
XX
PF   28-FEB-2003; 2003US-00377268.
XX
PR   28-FEB-2002; 2002US-0360651P.
PR   16-SEP-2002; 2002US-0411139P.
PR   20-SEP-2002; 2002US-0412341P.
PR   02-JAN-2003; 2003US-0437929P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
PI   Hirth K, Milburn MV;
XX
DR   WPI; 2004-642017/62.
XX
PT   Designing a ligand binding to a target molecule, comprises identifying as
PT   molecular scaffolds compounds binding to members of a molecular family,
PT   detecting orientation of scaffolds at a binding site of target, and
PT   synthesising ligand.
XX
PS   Disclosure; SEQ ID NO 9; 186pp; English.
XX
CC   The present invention relates to a method of designing a ligand binding
CC   to a target molecule. The method involves identifying as molecular
CC   scaffolds compounds binding to members of a molecular family, detecting
CC   orientation of scaffolds at a binding site of target, and synthesising
CC   ligand. The invention is useful for designing drug products and for
CC   designing ligand binding to target molecules such as nuclear hormone
CC   receptors, TNF receptors, G-protein coupled receptors, methyl
CC   transferases, ligases, etc. The present sequence is the human PIM 1
CC   protein. This sequence is used to illustrate the method of invention.
XX
SQ   Sequence 313 AA;

Query Match   98.1%; Score 1636; DB 8; Length 313;
Best Local Similarity   97.1%;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

```
RESULT 14
ADP24227
ID   ADP24227 standard; protein; 313 AA.
XX
AC   ADP24227;
XX
DT   18-NOV-2004  (first entry)
XX
DE   PRO polypeptide SEQ ID NO:1405.
XX
KW   PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW   osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW   antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
OS   Unidentified.
XX
PN   WO200404170-A2.
XX
PD   21-MAY-2004.
XX
PF   30-OCT-2003; 2003WO-US034312.
XX
PR   01-NOV-2002; 2002US-0423394P.
XX
PA   (GETH ) GENENTECH INC.
XX
PS   Claim 7; SEQ ID NO 1405; 2940pp; English.
XX
PT   New PRO polypeptides and polynucleotides, useful for treating e.g.
PT   erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT   renal disease, or demyelinating diseases of the central or peripheral
PT   nervous system.
XX
CC   The invention relates to a novel isolated nucleic acid and the PRO
CC   polypeptide encoded by it. A protein of the invention has
CC   antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC   osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC   antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC   of the invention may have a use in gene therapy. The PRO polypeptide, its
CC   agonist, antagonist, or antibody that specifically binds to the
CC   polypeptide is useful for treating an immune related disorder such as
CC   systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC   juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC   idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC   vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC   thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC   disease, a demyelinating disease of the central or peripheral nervous
CC   system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC   a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC   disease, infectious or autoimmune chronic active hepatitis, primary
CC   biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
```

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CC   inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC   disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC   disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC   disease, asthma, allergic rhinitis, atopic dermatitis, food
CC   hypersensitivity, urticaria, an immunologic disease of the lung,
CC   eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC   pneumonitis, a transplantation associated disease, graft rejection or
CC   graft-versus-host disease. The present sequence represents a PRO protein
CC   of the invention.
XX
SQ   Sequence 313 AA;

Query Match             98.1%;  Score 1636;  DB 8;  Length 313;
Best Local Similarity   97.1%;
Matches 304;  Conservative 6;  Mismatches 3;  Indels 0;  Gaps 0;

Qy          1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESGYQVGPLLGSGGFGSVYSGIRVAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESGYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240

Qy        241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
              ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              ||||||||||||||
Db        301 EIHLHSLSPGPSK 313
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RESULT 15
ADT07365
ID   ADT07365 standard; protein; 313 AA.
XX
AC   ADT07365;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Human protein #1 associated to anticancer compound screening method.
XX
KW   prophylactic-therapeutic agent; apoptosis inducing agent;
KW   anticancer agent; serine/threonine kinase Pim-1; cancer; solid tumour;
KW   human.
OS   Homo sapiens.
XX
PN   WO200409015B-A1.
XX
PD   21-OCT-2004.
XX
PF   05-APR-2004; 2004WO-JP004917.
XX
PR   03-APR-2003; 2003US-0459644P.
XX
PA   (ONCO-) ONCOREX INC.
XX
PI   Kobayashi M, Jian C;
XX
DR   WPI; 2004-748778/73.
DR   N-PSDB; ADT07366.
XX
PT   Screening for a prophylactic-therapeutic apoptosis inducing agent or
```

```
Db         121 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy         181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
Db         181 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy         241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
Db         241 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy         301 EIHLHSLSPGPSK 313
Db         301 EIHLHSLSPGPSK 313
```

```
CC   Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
XX
DR   WPI; 2004-419628/39.
DR   N-PSDB; ADP24226.
```

```
PT   enhancer of anticancer agent, comprises use of serine/threonine kinase
PT   Pim-1, its partial peptide or its salt.
XX
PS   Disclosure; SEQ ID NO 1; 93pp; Japanese.
XX
CC   The invention relates to a method of screening a prophylactic-therapeutic
CC   agent for an apoptosis inducing agent or an enhancer of an anticancer
CC   agent. The method involves the use of a serine/threonine kinase Pim-1,
CC   its partial peptide or its salt. Also disclosed is a kit for carrying out
CC   the method of the invention. The method is useful for screening a
CC   prophylactic-therapeutic agent for cancer. The method is also useful for
CC   prophylaxis and/or treatment of cancer, inducing apoptosis, treating a
CC   patient having a solid tumour that is resistant to an anticancer agent
CC   (induced by hypoxia), and for screening a substance that promotes or
CC   inhibits the activity of serine/threonine kinase Pim-1. The present
CC   sequence represents a human polypeptide relating to the present
CC   invention.
XX
SQ   Sequence 313 AA;

Query Match           98.1%;    Score 1636;  DB 8;   Length 313;
Best Local Similarity 97.1%;    Pred. No. 1.6e-155;
Matches 304;  Conservative  6;  Mismatches  3;  Indels  0;  Gaps  0;

Qy      1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
          ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||:|
Db      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
          ||||||||::|||:||||||||||||||||||:|||||||||||||||||||||||||||
Db    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy    301 EIHLHSLSPSPSK 313
          ||||||||:|||||
Db    301 EIHLHSLSPGPSK 313
```

Search completed: May 4, 2006, 05:24:47
Job time : 114.667 secs

OM protein - protein search, using sw model

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Run on: May 4, 2006, 05:19:22 ; Search time 20.3333 Seconds
                 (without alignments)
                 1481.107 Million cell updates/sec

Title: US-10-705-757-4
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRAAPCNDL..........LLPQATAEIHLHSLSPSPSK 313

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
                 Maximum Match 10%
                 Listing first 45 summaries

Database :   PIR 80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1668	100.0	313	1	S26298	protein kinase (EC
2	1636	98.1	313	1	TVHUP1	protein kinase (EC
3	1584	95.0	313	1	TVMSP1	protein kinase (EC
4	876.5	52.5	370	1	S55333	protein kinase pim
5	622	37.3	363	2	T22255	hypothetical prote
6	495	29.7	409	2	T14435	hypothetical prote
7	378	22.7	481	2	I49072	protein kinase - m
8	374	22.4	1101	2	S66730	hypothetical prote
9	374	22.4	1398	2	T13741	hypothetical prote
10	367	22.0	504	2	T10449	probable serine/th
11	366	21.9	1358	1	S33653	probable serine/th
12	361	21.6	512	1	JC1446	serine/threonine-s
13	357.5	21.4	798	2	JC7500	qik protein - chic
14	357	21.4	512	2	T52633	serine/threonine-s
15	357	21.4	651	2	S52244	p69Eg3 protein - A
16	356	21.3	511	1	A56609	serine/threonine-s
17	355	21.3	726	2	T33998	hypothetical prote
18	354.5	21.3	887	2	T20941	hypothetical prote
19	353.5	21.2	469	2	B84644	probable protein k
20	350.5	21.0	504	2	T07415	probable serine/th
21	350	21.0	512	2	T07788	probable serine/th
22	348.5	20.9	414	2	JN023	probable serine/th
23	348	20.9	472	2	B90100	SNF-related kinase
24	344	20.6	513	1	S6004	serine/threonine-s
25	336.5	20.2	445	2	T50802	serine/threonine p
26	336.5	20.2	489	2	T04862	probable serine/th
27	336	20.1	713	2	S27966	probable serine/th
28	336	20.1	1558	2	T29253	hypothetical prote
29	334.5	20.1	1518	2	S37928	probable purine nu
30	333.5	20.0	339	2	S56719	serine/threonine-s
31	333.5	20.0	746	2	S62365	SNF1-related prote
32	333	20.0	435	2	B84707	probable protein k
33	333	20.0	502	2	T02306	probable protein k
34	331.5	19.9	502	2	G86414	probable serine/th
35	330	19.8	461	2	T14822	probable serine/th
36	328	19.7	442	2	T48203	hypothetical prote
37	328	19.7	745	2	G01025	serine/threonine-s
38	326	19.5	591	2	S54788	serine/threonine p
39	325.5	19.5	774	2	I48609	calcium-stimulated
40	325	19.5	513	1	S60303	probable serine/th
41	325	19.5	1246	2	G89287	protein H39E23.1 [
42	324.5	19.5	423	2	T40224	protein kinase - f
43	323.5	19.4	713	2	T37886	probable serine/th
44	322.5	19.3	473	1	S59941	serine/threonine-s
45	321.5	19.3	480	2	A86427	probable serine/th

ALIGNMENTS

RESULT 1
S26298
protein kinase (EC 2.7.1.37) pim-1 - rat
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene pro
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S26298
R;Wingett, D.; Reeves, R.; Magnuson, N.S.
Nucleic Acids Res. 20, 3183-3189, 1992
A;Title: Characterization of the testes-specific pim-1 transcript in rat.
A;Reference number: S26298; MUID:92319652; PMID:1620615
A;Experimental source: testis
A;Note: testis-specific transcript is shorter and more stable than the somatic transcr
A;Accession: S26298
A;Molecule type: mRNA
A;Residues: 1-313 <WIN>
A;Cross-references: UNIPROT:P26794; UNIPARC:UPI000011AD6; EMBL:X63675; NID:g56902; PIR
A;Note: in testis may be involved in signal transduction events of normal germ cell mat
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncoge
C;Superfamily: kinase-related transforming protein; protein kinase homology <KIN>
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted
A;Function: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon

Query Match   100.0%; Score 1668; DB 1; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.6e-74;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy   301 EIHLHSLSPSPSK 313
             |||||||||||||
Db   301 EIHLHSLSPSPSK 313

```
Db            301 EIHLHSLSPSPSK 313

RESULT 2
TVHUP1
protein kinase (EC 2.7.1.37) pim-1 - human
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
A;Accession: JU0327; A46554; A27476; I58412
R;Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.
A;Title: Primary structure of the putative human oncogene, pim-1.
A;Reference number: JU0327; MUID:90382681; PMID:2205533
A;Accession: JU0327
A;Molecule type: DNA
A;Residues: 1-313 <REE>
A;Cross-references: UNIPROT:P11309; UNIPARC:UPI000001060; GB:M27903; NID:g189958; PIDN:
J. Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.
A;Title: Cloning and characterization of the human PIM-1 gene: a putative oncogene relat
A;Cell. Biochem. 35, 105-112, 1987
A;Reference number: A46554; MUID:88115604; PMID:3429489
A;Accession: A46554
A;Molecule type: mRNA
A;Residues: 1-313 <MEE>
A;Cross-references: UNIPARC:UPI000001060; GB:M24779; NID:g1667790; PIDN:AAA81553.1; PID
R;Zakut-Houri, R.; Hazum, S.; Givol, D.; Telerman, A.
A;Title: The cDNA sequence and gene analysis of the human pim oncogene.
Gene 54, 105-111, 1987
A;Reference number: A27476; MUID:87277423; PMID:3475233
A;Accession: A27476
A;Molecule type: mRNA
A;Residues: 1-14, 'RA', 17-313 <ZAK>
A;Residues: 1-313 <DOM>
A;Cross-references: UNIPARC:UPI000149876C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PID
R;Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.
Oncogene Res. 1 103-112, 1987
A;Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immunolo
A;Reference number: I58412; MUID:88217305; PMID:3329709
A;Accession: I58412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-313 <DOM>
A;Cross-references: UNIPARC:UPI000001060; GB:M54915; NID:g189961; PIDN:AAA36447.1; PID
A;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
C;Genetics:
A;Gene: GDB:PIM1
A;Cross-references: GDB:119495; OMIM:164960
A;Map position: 6p21.2-6p21.2
C;Introns: 28/2; 63/3; 80/3; 203/1; 262/1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Keywords: ATP; autophosphorylation; phosphoprotein; protein kinase homology
C;Superfamily: kinase-related transforming protein; protein kinase homology
F;36-290/Domain: protein kinase homology; phosphotransferase; proto-oncogene
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted

Query Match             98.1%;   Score 1636;  DB 1;   Length 313;
Best Local Similarity   97.1%;   Conservative     6;  Mismatches   3;  Indels   0;  Gaps   0;
Matches   304;

Qy       1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
           ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db       1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy      61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLI 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120

Qy     121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy     181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHYHGRSAAVWSLGILLYDMVCGDI 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHYHGRSAAVWSLGILLYDMVCGDI 240

Qy     241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQETA 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 PFEHDEEIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy     301 EIHLHSLSPSPSK 313
           |||||||||||||
Db     301 EIHLHSLSPSPSK 313

RESULT 3
TVMSP1
protein kinase (EC 2.7.1.37) pim-1 - mouse
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
A;Accession: A24169
R;Selten, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.; v
Cell 46, 603-611, 1986
A;Title: The primary structure of the putative oncogene pim-1 shows extensive homology w
A;Reference number: A24169; MUID:86272109; PMID:3015420
A;Accession: A24169
A;Molecule type: DNA
A;Residues: 1-313 <SEL>
A;Cross-references: UNIPROT:P06803; UNIPARC:UPI00000294AF; GB:M13945; GB:M13946; NID:g20
A;Comment: Pim-1 autophosphorylates at unknown sites.
C;Cross-references:
C;Genetics:
A;Gene: pim-1
C;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted

Query Match             95.0%;   Score 1584;  DB 1;   Length 313;
Best Local Similarity   94.2%;   Conservative     8;  Mismatches  10;  Indels   0;  Gaps   0;
Matches   295;

Qy       1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
           |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLLSKINSLAHLRRAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy      61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLI 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120

Qy     121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db     121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy     181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           ||||||||||||||||||||||||||||||:||:||:||||||||||||||||||||||
Db     181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRHYHGRSAAVWSLGILLYDMVCGDI 240

Qy     241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQETA 300
           ||||||||:|||:|||||||||||||:|||||||||||:||||||:||||||:||||:
Db     241 PFEIDEEIKGQVFFRQRVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy     301 EIHLHSLSPSPSK 313
           |||||||:||||
Db     301 EIHLHSLSPGSSK 313

RESULT 4
S55333
protein kinase pim-2 (EC 2.7.1.-) - mouse
```

```
C;Species: Mus musculus (house mouse)
C;Date: 10-Oct-1995 #sequence revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S55333; A43093; B43093
R;van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; van der Gulden, H.; Allen
  EMBO J. 14, 2536-2544, 1995
A;Title: Proviral tagging in E-mu-myc transgenic mice lacking the Pim-1 proto-oncogene 1
A;Reference number:
A;Accession: S55333
A;Molecule type: mRNA
A;Residues: 1-370 <VAN>
A;Cross-references: UNIPROT:Q62070; UNIPARC:UP100000028629; GB:L41495; NID:g9765065; PIDN:
A;Note: 40K form
A;Accession: A43093
A;Molecule type: mRNA
A;Residues: 'M',27-370 <VA2>
A;Cross-references: UNIPARC:UP100000278BE; GB:L41495; NID:g9765065; PIDN:AAA98923.1; PID:
A;Accession: B43093
A;Molecule type: mRNA
A;Residues: 'M',61-370 <VA3>
A;Cross-references: UNIPARC:UP100000278BF; GB:L41495; NID:g9765065; PIDN:AAA98924.1; PID:
A;Note: 34K form
A;Comment: Pim-2 autophosphorylates at unknown sites.
C;Genetics:
C;Gene: Pim-2
A;Gene: Pim-2
A;Map position: X
A;Start codon: CTG
A;Note: locus between A-raf and Act-7, near Kv4.1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotra
F;89-345/Domain: protein kinase homology <KIN>
F;97-105/Region: protein kinase ATP-binding motif
F;120/Active site: Lys #status predicted

Best Local Similarity  52.5%;          Score 876.5;  DB 1;   Length 370;
Matches 167;  Conservative 40;  Mismatches 74;  Indels  5;  Gaps  2;

Qy   28 GKEKEPLESQYQVGPLLGSGGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP 87
         ::| || ::|: |||| |:||||:| ||:||  :::||||  |  ::  |::  |||||
Db   81 GKDRAAFEAEYRLGPLLGKGGFGTVFAGHRVVTDRRQVAIKVISRNRVLGWSTVSDSVTCP 140

Qy   88 MEVVLLKKV--SSGFSGVIRLLDWFERPDSFVLILERREPVQDLFDFITERGALQEELAR 145
         :||::::|   :::: |||||||||  ||.|::::|| | :||||:|||:| :|| | :|
Db  141 LEVALIMKVGEGNGHPGVIRLLDWFETPEGFMLVLERPMPAQDLFDYITEKGPLGESCSR 200

Qy  146 SFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTR 205
         ||| ||: ||:|||  |:|||||||||||||| ||.:||||||||||| | .||||||||
Db  201 SFFTQVVAAVQHCHARGVVHRDIKDENILIDLCRGSIKLIDFGSGALLHDEPYTDFDGTR 260

Qy  206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEIVKGQVYFRQRVSSECQH 265
         ||||||| | : ||:  ||||||:||||||||||||||:|:||  : :|| :||::|  
Db  261 VYSPPEWISRHQYHALPATVWSLGVLLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA 320

Qy  266 LIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATAEIHLHSLSPSP 311
         ||| ||:  | .||| ||: :.|||| :||  ::  . :.| . |
Db  321 LIRRCLAPKPCSRPSLEEILLDPWMQS---PAEEKPINSSKGSPTP 363


RESULT 5
T22255
hypothetical protein F45H7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T22255
R;Percy, C.
  submitted to the EMBL Data Library, June 1994
R;Reference number: Z19538
A;Accession: T22255
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
```

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A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:Q20443; UNIPARC:UP100001755A4; EMBL:Z34800; PIDN:CAA84323.1
A;Experimental source: UNIPROT:Q20443; UNIPARC:UP100001755A4; EMBL:Z34800; PIDN:CAA84323.1
A;Gene: CESP:F45H7.4
A;Genetics:
A;Gene: CESP:F45H7.4
A;Map position: 3
A;Introns: 72/3; 160/3; 310/1
C;Superfamily: protein kinase homology

Query Match      37.3%;          Score 622;   DB 2;   Length 363;
Best Local Similarity  45.7%;    Pred. No. 1.1e-23;
Matches 121;  Conservative 49;  Mismatches 89;  Indels  6;  Gaps  3;

Qy   35 ESQYQVGPLLGSGGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLK 94
         : :| :| |||.||||.||| .:|  |:  ||||   :.|     |:||| :||| :  ||
Db   28 KKNYKLKAELGRGGFGVVYRAVRTCDNALVAVKPIERSNVKEWARI-NGEQVPMEICMLA 86

Qy   95 KVSSGFSGVIRLLDWFERPDSFVLILERREPVQDLFDFITERGALQEELARSFFWQVLEA 154
         | |:  .||||||||: :|: |::::|| | :|:||||| :|  |::::||.||| :  :
Db   87 KCSK-VRGVIRLLDWYSIPEGFLIVMERYPCIDMFDFIKQGRISEDMARFLFRQIAVT 145

Qy  155 VRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIR 214
         |: | : .|||||||||||:|| :| :||||||.:: | :: |: ||.||:| |||||:
Db  146 VHECVQNRVLHRDIKDENIVIDLVTGSTKLIDFGAATVLRRSQYSDFQGTRLYCPPEWFL 205

Qy  215 YHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI----VKGQVYFRQRVSSECQHLIRWC 270
         :  : ||.AAVWSLG:LL:: : |:.||.::: |     : .: : |: |:|  ||:| 
Db  206 HSLYLGRBAAVWSLGVLLYNSLNGRLPFRNEKDICTAHLLGPLPFFVPVSAEVKDLISKC 265

Qy  271 LSLRPSDRPSFEEIQNHPWMQDVLL 295
         |:  |.:||: ||| |||||:: 
Db  266 LTFDPFQRCSLEAILNHPWVKQQTL 290


RESULT 6
T15435
hypothetical protein C06E8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15435
R;Favello, A.
  submitted to the EMBL Data Library, February 1994
A;Description: The sequence of C. elegans cosmid C06E8.
A;Reference number: Z18350
A;Accession: T15435
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-409 <FAV>
A;Cross-references: UNIPARC:UP10000017B744; EMBL:U00034; NID:g458983; PID:g458986; PIDN:
A;Experimental source: strain Bristol N2
A;Genetics:
A;Gene: CESP:C06E8.3
A;Molecule type: DNA
A;Introns: 24/1; 76/3; 107/2; 145/3; 199/1; 307/1; 375/1
A;Gene: CESP:C06E8.3

Query Match      29.7%;          Score 495;   DB 2;   Length 409;
Best Local Similarity  35.3%;    Pred. No. 1.6e-17;
Matches 110;  Conservative 57;  Mismatches 129;  Indels 16;  Gaps  6;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGGFGSVYSGIRVAD 60
          : |: : |:    ||:| | :. :  .|:|  |: | :|  |||.|||||.|:||
Db    1 MIRKLQDLAVCCSYQVDFLHEKK----HSVKEFKRKYEVLDEIGRGGFGFGIVVEAATRQD 56

Qy   61 -NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLI 119
           :|||:|  |:  |    : ::: : |.|::  :  : . .|||||:||||  | .|:|
Db   57 GQQPVAVKFVQHGHVRSW-TMTCRQLIPSEVCHL-ETCEDIPGVIKILDWFANSKGFIV 114

Qy  120 LERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHN-CGVLHRDIKDENILIDLN 178
         :|||   |||||::. | : :|:: :.: : ||   :: :.  .:|||||||||:|:  |
Db  115 MERPANCMDLFDMVSHGPLNEDMGKFIFKQVTTVFNMYSKHGLLHRDIKDENLIVAMN 174

Qy  179 RGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG 238
          ||:|||.|||.| .::::   .:|||.| |||||:   :|:::.|||||||:|::::.|
Db  175 TGEVKLIVDFGATAYAEKATKKEFQGTRSYCPPEWFRDQLYLPLEATSWSLGVLFILITG 234
```

RESULT 7
I49072
protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996
C;Accession: I49072
R;Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A;Title: Identification of novel protein kinases expressed in the myocardium of the deve
A;Reference number: I49071; MUID:95200798; PMID:7893599
A;Accession: I49072
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-481 <RES>
A;Cross-references: UNIPARC:UPI000017A422; EMBL:U11494; NID:g595420; PIDN:AAA67926.1; PI
F;71-324/Domain: protein kinase homology <KIN>
F;79-87/Region: protein kinase ATP-binding motif

Query Match   22.7%; Score 378; DB 2; Length 481;
Best Local Similarity 33.2%; Pred. No. 8.4e-12;
Matches 97; Conservative 53; Mismatches 116; Indels 26; Gaps 10;

```
Qy    9 LAHLRAAPCNDLHANKLAPGKEKEPLE-SQYQVGPLLGSSGGFGSV-YSGIRVADNLPVAI 66
          :   :    :: ::::   :   : ::  :: :  :
Db   51 MSEFRAVPS--------GTGRSQKPLRVGVGFYDVERTLGKGNFAVVKLGRGHRVT-KTQVAI 101

Qy   67 KHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLILERPEPV 126
          : ::: : ::     :: :::   ::   :  : :: :::
Db  102 KIIDKTRL-----DSSNLEKIYREVQLMKLLN--HPNIIKLYQVWETKDMLIYTEFAKN- 154

Qy  127 QDLLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENIIIDLNRGELKLID 186
         :  :: ::   ::     : ::::: :  :  ::: :: :: :::  :  :: :
Db  155 GEMFDYLTSNGHLSENEARQKFWQILSAVEYCHNHHIVHRDLKTENLLLDSNM-DIKLAD 213

Qy  187 FGSGALLK-DTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILILYDMVCGDIPFEHD 245
         ::   :   :   :  : : :   ::     ::  :: :: :: : :  ::::::::
Db  214 FGFGNFYKPGEPLSTCVSSPYYAAPEVFEGKEYEGPQLDVWSLGVVLYLVLCCGSLPFDGP 273

Qy  246 -----EEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQ 291
              : ::: ::      :  :  : ::: ::::: :  ::::::::::
Db  274 NLPTLRQRVLEGRFRIPFFMSQDCETLIRRMLVVDPAKRITIAQIRQHRWMQ 325
```

F;839-1099/Domain: protein kinase homology <KIN>
F;847-855/Region: protein kinase ATP-binding motif

RESULT 8
S66730
hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2034
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Oct-2004
C;Accession: S66730
R;Ansorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wiemann, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66723
A;Accession: S66730
A;Molecule type: DNA
A;Residues: 1-1101 <ANS>
A;Cross-references: UNIPROT:Q08217; UNIPARC:UPI00012DF35; EMBL:Z74788; NID:g1419846; PI

Query Match   22.4%; Score 374; DB 2; Length 1101;
Best Local Similarity 32.2%; Pred. No. 2.6e-11;
Matches 86; Conservative 62; Mismatches 103; Indels 16; Gaps 6;

```
Qy   36 SQYQVGPLLGSSGGFGSVYSGIRVADNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLL 93
         :  :  : :::  : ::    :   :: :  : ::::: :     : ::  :  :
Db  839 SDFTILQVWGEGAYGKVVNLCIIHNREHYIVVIKMFKERILVDDTWVRDRKLGTIPSEIQIM 898

Qy   94 KKVS-SGFSGVIRLLDWFERPDSFVLILERPEPVQ------DLFDFITERGALQEELARS 146
         :     : :: ::: :::  :  : : :  :        :: ::   ::    : :
Db  899 ATLNKNSQENILKLLDFEDDYYI---ETPVHGETGSIDLFDVIEFKKDMVEHEAKL 954

Qy  147 FFWQVLEAVRHCHNCGVLHRDIKDENIIIDLNRGELKLIDFGSSGALLKDTVYTDFDGTRV 206
         :::: :: :  :: : :::::::::::  : : :::::::::    : ::::: :  ::
Db  955 VFKQVVASIKHLHDQGIVHRDIKDENVIVD-SHGFVKLIDFGSAAYIKSGPFDVFVGTMD 1013

Qy  207 YSPPEWIRYHRYHGRSAAVWSLGILILYDMVCGDIPFEHDEEIVKGQVYF--RQRVSSECQ 264
          : ::      :  :::  : ::::: ::  :::::::::  :: :  :    ::  ::
Db 1014 YAAPEVLGGSSYKGKPQDIWALGVLLYTIIYKENPYYNIDEILEGELRFDKSEHVSECI 1073

Qy  265 HLIRWCLSLRPSDRPSFEEIQNHPWMQ 291
          ::   :     : ::::  :  : :
Db 1074 SLIKRILTREVDKRPTIDEIYEDKWLK 1100
```

RESULT 9
T13741
hypothetical protein 22E5.8 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13741
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17668
A;Accession: T13741
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1398 <MUR>
A;Cross-references: UNIPROT:O77268; UNIPARC:UPI00000820A3; EMBL:AL031765; NID:e1371523;
A;Genetics:
C;Cross-references: FlyBase:FBgn0000667
A;Introns: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3
A;Note: EG:22E5.8

Query Match   22.4%; Score 374; DB 2; Length 1398;
Best Local Similarity 33.0%; Pred. No. 3.2e-11;
Matches 91; Conservative 57; Mismatches 110; Indels 18; Gaps 9;

```
Qy   29 KEKEPLE-SQYQVGPLLGSSGGFGSV-YSGIRVADNLPVAIKHVEKDRISDWGELPNGTRV 86
          :::    :  : : :::    : :   :: :  :: :  : : :::   :
Db  131 KLKEPMRVGFYDIERTIGKGNFAVVKLARHRITKN-EVAIKIIDKSQL---DQTNLQKV 185

Qy   87 PMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARS 146
          :::   :     : :: ::: ::: :    : : ::     ::  :
Db  186 YREVEIMKRLK--HPHIIKLYQVWETKNMIYIVSEYASQ-GEIFDYIAKYGRMSESAARF 242

Qy  147 FFWQVLEAVRHCHNCGVLHRDIKDENIIIDLNRGELKLIDFG-SGALLKDTVYTDFDGTR 205
         :::: :: :  :: : :::::::::::  : : ::::::::: :  : ::
Db  243 KFWQIISAVEYCHKKGIVHRDLKAENLLLDLNM-NIKIADFGFSNHFKPGELLATWCGSP 301

Qy  206 VYSPPEWIRYHRYHGRSAAVWSLGILILYDMVCGDIPFEHD------EEIVKGQVYFRQRV 259
           : ::      :  :::  : ::::: ::  :::::::::       :: : :    :
Db  302 PYAAPEVEGKQYTGPEIDIWSLGVVLYVLVCGALPFDGSTLQSLRDRVLSGRFRIPFFM 361

Qy  260 SSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQODVLL 295
         ::::  :: :  :     : :::  :  : :
Db  362 SSECHLIRRMLVLEPTRRYTIDQIKRHRWMCPELL 397
```

RESULT 10
T10449
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N;Alternate names: SNF1-related protein kinase
C;Species: Cucumis sativus (cucumber)
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-504 <GUM>
A;Cross-references: UNIPROT:P93113; UNIPARC:UPI00000A4B92; EMBL:Y10036
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-Oct-2004
C;Accession: T10449
R;Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
R;Reference number: Z17020
A;Accession: T10449
A;Reference number: T10449
A;Experimental source: cv. Masterpiece; cotyledon
C;Genetics:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>

Query Match
Best Local Similarity   22.0%;
Matches 90; Conservative 51;   Score 367; DB 2; Length 504;
                                   Pred. No. 3e-11; Mismatches 105; Indels 16; Gaps 8;

Qy 38 YQVGPLLGSGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
        |||::|:|:|||:|||:||:|||| || ||||||| :: | || ||||||||:|||||||
Db   8 YKLGKTLGIGSFGKVKIAEHALTGHKVAIKILNRRKIKN---LDMEEKVRREIKILRLFM 64

Qy 98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
         .:|||:||||:||||||:||:||:||:: : |:|:|.||:||:||||:|::|::|:
Db 65 --HPHIIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 121

Qy 158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGGSGALLKDTVYTDFD-GTRVYSPPEWIRYH 216
        || :|:|||:|.|||:|| |.:||| ||||.|||:|||||| |:| || |||||||||
Db 122 CHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 180

Qy 217 RYHGRSAAVWSLGILLLYDMVCGDIPFEHDEEI------VKGQVY-FRQRVSSECQHLIRW 269
         | | | :|:| :||:|:::||:|||: |:.:   .|| :| : |:|| | ::
Db 181 LYAGPEVDVSWSCCVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELIPS 239

Qy 270 CLSLRPSDRPSFEEIQNHPWMQ 291
         : |:|.|:| |::|||::|
Db 240 MLVDPMKRITIPEIRQHPWFQ 261

A;Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcription
R;Reference number: S22266; MUID:92221690; PMID:1561836
A;Accession: S36732
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-862 <CL2>
A;Cross-references: UNIPROT:UPI000017A44A; EMBL:S93805
R;Sidhu, R.S.; Mathews, S.; Bollon, A.P.
Gene 107, 111-118, 1991
A;Cross-references: UNIPROT:UPI000017A44B
A;Accession: JH0486
A;Reference number: JH0483; MUID:92077420; PMID:1743509
A;Title: Selection of secretory protein-encoding genes by fusion with PHO5 in Saccharo
A;Accession: JH0486
A;Molecule type: DNA
A;Residues: 1-72, E',74-154 <SID>
A;Cross-references: UNIPARC:UPI00000A4B92
A;Gene: SGD:FUN31;
C;Cross-references: SGD:S0000015; MIPS:YAL017w
A;Map position: 1L
C;Superfamily:
C;Keywords: ATP; Glycoprotein; phosphotransferase; serine/threonine-specific protein ki
F;1096-1356/Domain: protein kinase homology <KIN>
F;1104-1112/Region: protein kinase ATP-binding motif
F;8,128/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1232/Active site: Asp #status predicted

RESULT 11
S33653
probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 02-Aug-1994 #text_change 05-Oct-2004
C;Accession: S33653; S36717; S36732; JH0486
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kaba
A;Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae enc
Yeast 9, 543-549, 1993
R;Reference number: S33653; MUID:9311122; PMID:8322517
A;Accession: S33653
A;Molecule type: DNA
A;Status: nucleic acid sequence not shown
A;Accession: S36717
A;Molecule type: DNA
A;Reference number: S36711
A;Description: Sequencing of chromosome I from Saccharomyces cerevisiae: analysis of a 3
R;Ouellette, B.F.F.; Clark, F.J.; Keng, T.; Storms, R.K.; Zhong, W.W.; Zeng, B.; Fortin, N.; D
A;Cross-references: UNIPROT:P31374; UNIPARC:UPI000017A449; EMBL:L05146
A;Molecule type: DNA
A;Residues: 1-1358 <CLA>

Query Match
Best Local Similarity   21.9%;
Matches 86; Conservative 56;   Score 366; DB 2; Length 1358;
                                   Pred. No. 7.7e-11; Mismatches 100; Indels 16; Gaps 6;

Qy 44 LGSGGFGSSVYSGIRVADNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLLKKVS-SGF 100
        :|.|.:| | . |: . .:.| :| : .|| :| | || |. :| :| .: ..| ||
Db 1104 MGEGAYGKVNLCIHKKNRVIVIVRKMFKERILVDDTWVRDRKLGTIPSEIQIMATLNKKPH 1163

Qy 101 SGVIRLLDWFERPDSFVLILERPEPVQ-----DLFDFITERGALQEELARSFFWQVLEA 154
         ..:|||| |: .| :. | | :| |||: |.|:| :|:| : :: |: |
Db 1164 ENILRLLDFFEDDDYYI----ETPVHGETGCILFDLLEFKTNWTEFEAKLIFKQVVAG 1219

Qy 155 VRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGGSGALLKDTVYTDFDGTRVYSPPEWIR 214
         :: || |:|||||||| :.| .|.||:|||||.|| ||.:   : :| .|:||||:|
Db 1220 IKIHLHDQGIVHRDIKDENVIVD-SKGFVKIIDFGGSAAYVKSGPEDVFVGTIDYAAPEVLG 1278

Qy 215 YHRYHGRSAAVWSLGILLLYDMVCGDIPFEHDEEIVKGQVYFR--QRVSSECQHLIRWCLS 272
          .| | : :|::|||| | .| |::|||:.:|:.||| ||| || | || :|:||:|
Db 1279 GNPYEGPQPDIWAIGILLYTVVFKENPFYNIDEILEGDLKFNNAEEVSEDCIELIKSILN 1338

Qy 273 LRPSDRPSFEEIQNHPWM 290
         |. || :..|:| ||
Db 1339 RCVPKRPTIDDINNDKWL 1356

RESULT 12
JC1446
serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana
N;Alternate names: protein kinase SNF1 homolog
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Oct-2004
C;Accession: JC1446; S58266; S66334
R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
R;Reference number: JC1446; MUID:93013041; PMID:1339373
A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protei
A;Accession: JC1446
A;Reference number: JC1446
A;Molecule type: DNA
A;Residues: 1-512 <LEG>
R;Thuemmler, F.; Kircher, M.; Teuber, R.; Dittrich, P.
submitted to the EMBL Data Library, May 1995
A;Description: Differential accumulation of the transcripts of 22 novel protein kinase
R;Reference number: S58256
A;Accession: S58266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 144-198 <THU>

A;Cross-references: UNIPARC:UPI000009DEE0; EMBL:X86966; NID:g9928909; PIDN:CAA60529.1; PI
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
A;Cross-references: UNIPARC:UPI000009DEE0; EMBL:X86966; NID:g9928909; PIDN:CAA60529.1; PI
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes i
A;Reference number: S66314; MUID:96123233; PMID:8534852
A;Accession: S66334
A;Molecule type: DNA
A;Residues: 144-198 <TH2>
A;Comment: This enzyme plays an important role in a signal transduction cascade regulati
C;Superfamily: SNF1-related protein kinase; protein kinase homology
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Keywords: ATP; magnesium; phosphotransferase; protein kinase; serine/threonine-specific protein kinase
A;Gene: AKin10; AK21
A;Intron: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
F;25-33/Region: protein kinase ATP-binding motif
F;147,151/Binding site: magnesium (Asn, Asp)
F;17-271/Domain: protein kinase homology <KIN>
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted

Best Local Similarity   21.6%;   Score 361;   DB 1;   Length 512;
Query Match   33.6%;   Pred. No. 5.9e-11;
Matches   90;   Conservative   51;   Mismatches 111;   Indels   16;   Gaps   8;

Qy   32   EPLESQYQVGPLLGSGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV 91
Db   26   YDIERTLGKGNFAVVKLARHRVTKTQVAIKIIDKTRL----DPSNLEKIYREVOIMKLLN 81
Qy   92   LLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQV 151
Db   82   --HPHIIKLYQVMETKDMLYIVTEFAKN-GEMFDHLTSNGHLSESEARKKFWQILSAVEY 138
Qy   152   LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSSGALLKDTVYTDFD-GTRVYSPP 210
Db   139   CHSHHIVHRDLKTENLLLDANM-NIKLADFGFGNFYKSGEPLSTWCGSPPYAPEVFEGK 197
Qy   211   EWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----VKGQVY-FRQRVSSEC 263
Db   198   EYGGHPLDIWSLGVVLYVLVCGSLPFDGPNLPLRQRVLEGRFRIPYFYEMSEDCETLIRM 257
Qy   264   QHLIRWCLSLRPSDRPSFEEIQNHPWMQ 291
Db   258   LVVDETKRITISQIKQHKWMQ 278

RESULT 14

T52633
serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN11 [validated] - Arabidopsis t
N;Alternate names: SNF1 protein kinase omolog AKIN11
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 05-Oct-2004
C;Accession: T52633
R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machid
A;Title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNF1-like protein ki
A;Reference number: Z25116; MUID:99238528; PMID:10220464
A;Accession: T52633
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-512 <BHA>
A;Cross-references: UNIPROT:P92958; UNIPARC:UPI00000AC16D; EMBL:X99279; PIDN:CAA67671.1
A;Experimental source: cultivar Columbia
A;Gene: AKIN11
C;Function: EC 2.7.1.-; serine/threonine-specific protein kinase
A;Description: complements SNF1 mutations in yeast
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Best Local Similarity   21.4%;   Score 357;   DB 2;   Length 512;
Query Match   33.6%;   Pred. No. 9.2e-11;
Matches   90;   Conservative   52;   Mismatches 110;   Indels   16;   Gaps   8;

Qy   32   EPLESQYQVGPLLGSGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV 91
Db   14   ESILPNYKLGKTLGIGSFGKVKIAEHVTGHKVAIKILNRRKIN---MEMEKVRREIK 70
Qy   92   LLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQV 151
Db   71   ILRLFM--HPHIIRQYEVIETTSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQI 127
Qy   152   LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSSGALLKDTVYTDFD-GTRVYSPP 210
Db   128   ISGVEYCHRNMVVHRDLKPENLLD-SRCNIKIADFGLSNIMRDGHFLKTSCGSPNYAAP 186
Qy   211   EWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----VKGQVY-FRQRVSSEC 263
Db   187   EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSEA 245
Qy   264   QHLIRWCLSLRPSDRPSFEEIQNHPWMQ 291
Db   246   RDLIPRMLIVDPVKRITIPEIRQHRWFQ 273

RESULT 15

S52244
p69Eg3 protein - African clawed frog

Qy   38   YQVGPLLGSGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97

RESULT 13

JC7500
qik protein - chicken
N;Alternate names: Qin-induced kinase
C;Species: Gallus gallus (chicken)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7500
R;Xia, Y.; Zhang, Z.; Kruse, U.; Vogt, P.K.; Li, J.
A;Title: The new serine-threonine kinase, Qik, is a target of the qin oncogene.
A;Reference number: JC7500
A;Contents: Embryo fibroblasts
A;Accession: JC7500
A;Molecule type: mRNA
A;Residues: 1-798 <XIA>
A;Cross-references: UNIPROT:Q9I0A88; UNIPARC:UPI00000044792; GB:AF219232
A;Description: This protein, a member of the AMPK/SNF1 family of serine/threonine kinases, t
C;Genetics:
A;Gene: qik
C;Keywords: protein kinase

Best Local Similarity   21.4%;   Score 357.5;   DB 2;   Length 798;
Query Match   32.2%;   Pred. No. 1.3e-10;
Matches   84;   Conservative   51;   Mismatches 111;   Indels   15;   Gaps   6;

Qy   32   EPLESQYQVGPLLGSGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV 91
Db   13   ESILPNYKLGRTLGIGSFGRVKIAEHALTGHKVAIKILNRRKIN---MEMEKVRREIK 69
Qy   70   ILRLFM--HPHIIRLYEVIETPTDIYLVMEYVNS-GELFDYIVEKGRLQEDEARNFFQQI 126
Qy   92   LLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQV 151
Qy   152   LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSSGALLKDTVYTDFD-GTRVYSPP 210
Db   127   ISGVEYCHRNMVVHRDLKPENLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAP 185
Qy   211   EWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----VKGQVY-FRQRVSSEC 263
Db   186   EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSPCA 244
Qy   264   QHLIRWCLSLRPSDRPSFEEIQNHPWMQ 291
Db   245   RDLIPRMLVVDPMKRVTIPEIRQHPWFQ 272

```
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: S52244
R;Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A;Description: Eg3, selected by differential screening encodes a new Xenopus protein kin
A;Reference number: S52243
A;Accession: S52244
A;Accession: S52243
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-651 <ROG>
A;Cross-references: UNIPROT:Q91821; UNIPARC:UPI000017A463; EMBL:Z17205; NID:g609283; PID
C;Keywords: ATP
F;11-265/Domain: protein kinase homology <KIN>
F;19-27/Region: protein kinase ATP-binding motif

Query Match       21.4%;   Score 357;   DB 2;   Length 651;
Best Local Similarity  34.1%;   Pred. No. 1.1e-10;
Matches  92;  Conservative  53;  Mismatches 103;  Indels  22;  Gaps  8;

Qy    32 EPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV   91
            | |:    :|:|||| |                        :: |||  :|
Db     7 EELLKYYELHETVGTGGFAKVKLASHLITGEKVAIKIMDKESLGD--DLP---RVKTEID   61

Qy    92 LLKKVSSGFSGVIRLLDWFERPDSFVLLERPEPVQDLLFDFITERGALLQEELARSFFWQV   151
           |:||       | |    ||:|||:|:|  |  |||:    :|   |||:
Db    62 AMKNLS--HQHVCRLYHVIETPKKIFMVLEYC-PGGELFDYIIAKDRLTEEEARVFFRQI   118

Qy   152 LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-----GTRV   206
          : ||: | :  |:|||||| ||:||::|   |||||||      | |         ||:
Db   119 VSAVAYIHSQGYAHRDLKPENLLIDEDQ-NLKLIDFGLCAKPKGGL--DYHLMTCCGSPA   175

Qy   207 YSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD-------EEIVKGQVYFRQRVS   260
          | |  | | | | :      | | | |||:  | |:|:          ::||:|:  :|
Db   176 YAAPELIQGKAYIGSEADIWSMGVLMYALMCGYLPFDDDNVMVLYKKIMRGKYEIPKWLS   235

Qy   261 SECQHLIRWCLSLRPSDRPSFEEIQNHPWM  290
            | :  :    : : ||| |||:
Db   236 PGSVLLLSQMMQVDPKKRITVKHLLNHPWL  265
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Search completed: May 4, 2006, 05:25:52
Job time : 21.3333 secs

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OM protein - protein search using sw model

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GenCore version 5.1.7

Run on: May 4, 2006, 05:12:40 ; Search time 122 Seconds
(without alignments)
1810.085 Million cell updates/sec

Title: US-10-705-757-4
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRAAPCNDL.........LLPQATAEIHLHSLSPSPSK 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1668	100.0	313	1	PIM1_RAT	P26794 rattus norv
2	1658	98.2	313	1	PIM1_FELCA	Q95J0 felis silve
3	1636	98.1	313	1	PIM1_HUMAN	P11309 homo sapien
4	1636	98.1	313	2	Q5T7H7_HUMAN	Q5t7h7 homo sapien
5	1630	97.7	313	1	PIM1_BOVIN	Q8nop9 bos taurus
6	1589	95.3	313	2	Q8CFN8_MOUSE	Q8cfn8 mus musculu
7	1584	95.0	313	1	PIM1_MOUSE	P06803 mus musculu
8	1137	68.2	323	1	PIM1_COTJA	Q9pu85 coturnix co
9	1135	68.0	326	1	PIM1_HUMAN	Q86V86 homo sapien
10	1132.5	67.9	326	1	PIM3_MOUSE	P58750 mus musculu
11	1132.5	67.9	326	1	PIM3_RAT	O70444 rattus norv
12	1131.5	67.8	326	1	PIM3_RAT	Q4V8M2 rattus norv
13	1131.5	67.8	380	2	Q4V8M2_RAT	Q4v8m2 rattus norv
14	1119	67.1	325	2	Q811X8_MOUSE	Q811x8 mus musculu
15	1110.5	66.6	318	1	PIM3_XENTR	Q6III1_XENTR rattus norv
16	1102.5	66.1	323	1	PIM3_XENLA	Q91822 xenopus lae
17	1102.5	66.1	323	2	Q5U489_XENLA	Q5u489 xenopus lae
18	1098	65.8	337	2	Q4STF0_TETNG	Q4stf0 tetraodon n
19	1053	63.1	316	2	Q8R2P0_MOUSE	Q8r2p0 mus musculu
20	876.5	52.5	311	2	PIM2_MOUSE	Q62070 mus musculu
21	876.5	52.5	370	1	PIM2_MOUSE	Q9plw9 homo sapien
22	866.5	51.9	311	1	PIM2_HUMAN	Q7zvj5 brachydanio
23	861	51.6	310	2	Q7ZVJ5_BRARE	Q8jfw9 brachydanio
24	858	51.4	310	2	Q8JFW9_BRARE	Q9yhz5 brachydanio
25	853	51.1	310	1	PIM1_BRARE	Q6dl52 brachydanio
26	851	51.0	310	2	Q6DL52_BRARE	Q4tdc2 tetraodon n
27	796.5	47.8	288	2	Q4TDC2_TETNG	Q8r1z0 mus musculu
28	716.5	43.0	221	2	Q8R1Z0_MOUSE	Q61jb7 caenorhabdi
29	628	37.6	500	2	Q61JB7_CAEBR	Q20443 caenorhabdi
30	622	37.3	441	2	Q20443_CAEEL	Q61228 caenorhabdi
31	506	30.3	566	2	Q61228_CAEBR	Q8t3f1 caenorhabdi
...	506	30.3	566	2	Q8T3F1_CAEEL	Q8t3f1 caenorhabdi
...	495	29.7	378	2	Q8T3F1_CAEEL	Q17737 caenorhabdi
...	495	29.7	566	2	Q17737_CAEEL	Q17737 caenorhabdi

ALIGNMENTS

RESULT 1
PIM1_RAT

32	440	26.4	270	2	Q5SPE4_BRARE Q5spe4 brachydanio
33	421	25.2	416	2	Q4RFY6_TETNG Q4rfy6 tetraodon n
34	421	25.2	465	2	Q5SPF6_BRARE Q5spf6 brachydanio
35	419.5	25.1	134	2	Q6P2J9_HUMAN Q6p2j9 homo sapien
36	409	24.5	281	2	Q5SV44_BRARE Q5sv44 brachydanio
37	403	24.2	125	2	Q6Q2K5_CANFA Q6q2k5 canis famil
38	393.5	23.6	268	2	Q5SPP9_BRARE Q5spp9 brachydanio
39	391	23.4	1385	2	Q5PQT0_BRARE Q5pqt0 rattus norv
40	390.5	23.4	578	2	Q5RH93_BRARE Q5rh93 brachydanio
41	390	23.4	1383	1	PASK_MOUSE Q641K5 mus musculu
42	388.5	23.3	658	2	Q641K5_MOUSE Q641k5 mus musculu
43	384.5	23.1	261	2	Q5SPP7_BRARE Q5spp7 brachydanio
44	384.5	23.1	261	2	Q5SPQ2_BRARE Q5spq2 brachydanio
45	384	23.0	463	2	Q5RG24_BRARE Q5rg24 brachydanio

PIM1_RAT STANDARD; PRT; 313 AA.

ID PIM1_RAT STANDARD; PRT; 313 AA.
AC P26794;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN Name=Pim1; Synonyms=Pim-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=92319652; PubMed=1620615;
RA Wingett D.; Reeves R.; Magnuson N.S.;
RT "Characterization of the testes-specific pim-1 transcript in rat.";
RL Nucleic Acids Res. 20:3183-3189(1992)
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Binds to RP9 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -!- PTM: Autophosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC -!-
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -!-
DR EMBL; X63675; CAA45214.1; -; mRNA.
DR PIR; S26298; S26298.
DR SMR; P26794; 32-308.
DR Ensembl; ENSRNOG00000000529; Rattus norvegicus.
DR RGD; 3330; Pim1.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 38 290 Protein kinase.
FT NP_BIND 44 52 ATP (By similarity).
FT ACT_SITE 167 167 Proton acceptor (By similarity).
FT BINDING 67 67 ATP (By similarity).
SQ SEQUENCE 313 AA; 35631 MW; D5757DA9F1821BF9 CRC64;

RESULT 2

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Query Match        100.0%;
Best Local Similarity  100.0%;
Score 1668; DB 1; Length 313;
Best Local Similarity  100.0%;  Pred. No. 3.2e-115;
Matches  313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy 301 EIHLHSLSPSPSK 313
        |||||||||||||
Db 301 EIHLHSLSPSPSK 313
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```
ID   PIM1_FELCA     STANDARD;      PRT;   313 AA.
AC   Q9SLJ0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fujino Y., Satoh H., Hisasue M., Masuda K., Ohno K., Tsujimoto H.;
RT   "The cDNA sequence of the feline pim-1 oncogene.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; AB073748; BAB71752.1; -; mRNA.
DR   SMR; Q9SLJ0; 32-308.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
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RESULT 3

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Query Match        98.2%;
Best Local Similarity  97.4%;  Score 1638; DB 1; Length 313;
Matches  305;  Conservative  4;  Mismatches  4;  Indels  0;  Gaps  0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        |||||||||||||:||||||||||:||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRTRAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||:.||||:|||||||||||||||||:|||||||||||||||||||||||||:||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPSFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPSPSK 313
        ||||||||:||||
Db 301 EIHLHSLSPGPSK 313
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ID   PIM1_HUMAN     STANDARD;      PRT;   313 AA.
AC   P11309; Q96RG3;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=90382681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
RA   Reeves R., Spies G.A., Kiefer M., Barr P.J., Power M.;
RT   "Primary structure of the putative human oncogene, pim-1.";
RL   Gene 90:303-307(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88217305; PubMed=3329709;
RA   Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
RA   Berns A.;
RT   "Comparison of the human and mouse PIM-1 cDNAs: nucleotide sequence
RT   and immunological identification of the in vitro synthesized PIM-1
RT   protein.";
RL   Oncogene Res. 1:103-112(1987).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
RA   Zakut-Houri R., Hazum S., Givol D., Telerman A.;
RT   "The cDNA sequence and gene analysis of the human pim oncogene.";
RL   Gene 54:105-111(1987).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
FT   DOMAIN       38    290       Protein kinase.
FT   NP_BIND      44     52       ATP (By similarity).
FT   ACT_SITE    167    167       Proton acceptor (By similarity).
FT   BINDING      67     67       ATP (By similarity).
SQ   SEQUENCE   313 AA;  35686 MW;  C0BE268D63B86967 CRC64;
KW   Transferase.
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RX   MEDLINE=88115604; PubMed=3429489;
RA   Meeker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
RT   "Cloning and characterization of the human PIM-1 gene: a putative
RT   oncogene related to the protein kinases.";
RL   J. Cell. Biochem. 35:105-112(1987).
RN   [5]
RP   TISSUE=Kidney;
RC   TISSUE=Kidney;
CC   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   NUCLEOTIDE SEQUENCE OF 1-202.
RX   MEDLINE=21154098; PubMed=11460166; DOI=10.1038/35085588;
RA   Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
RA   Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
RT   "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
RT   cell lymphomas.";
RL   Nature 412:341-346(2001).
RN   [7]
RP   CHARACTERIZATION.
RX   MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
RA   Koike N., Maita H., Taira T., Ariga H., Iguchi-Ariga S.M.M.;
RT   "Identification of heterochromatin protein 1 (HP1) as a
RT   phosphorylation target by Pim-1 kinase and the effect of
RT   phosphorylation on the transcriptional repression function of HP1.";
RL   FEBS Lett. 467:17-21(2000).
RN   [8]
RP   FUNCTION.
RX   MEDLINE=22567470; PubMed=12680209;
RA   Ionov Y., Le X., Tunquist B.J., Sweetenham J., Sachs T., Ryder J.,
RA   Johnson T., Lilly M.B., Kraft A.S.;
RT   "Pim-1 protein kinase is nuclear in Burkitt's lymphoma: nuclear
RT   localization is necessary for its biologic effects.";
RL   Anticancer Res. 23:167-178(2003).
RN   [9]
RP   FUNCTION.
RX   MEDLINE=88246418; PubMed=2837645;
RA   Telerman A., Amson R., Zakut-Houri R., Givol D.;
RT   "Identification of the human pim-1 gene product as a 33-kilodalton
RT   cytoplasmic protein with tyrosine kinase activity.";
RL   Mol. Cell. Biol. 8:1498-1503(1988).
CC   -!- FUNCTION: Thought to play a role in signal transduction in blood
CC       cells. May affect the structure or silencing of chromatin by
CC       phosphorylating HP1 gamma/CBX3.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC   -!- TISSUE SPECIFICITY: Expressed primarily in cells of the
CC       hematopoietic and germ line lineages.
CC   -!- PTM: Autophosphorylated on tyrosine residues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PIMID261.html".
```

```
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; M27903; AAA60090.1; -; Genomic_DNA.
DR   EMBL; M16750; AAA60089.1; -; Genomic_DNA.
DR   EMBL; M54915; AAA36447.1; -; mRNA.
DR   EMBL; M24779; AAA81555.1; -; mRNA.
DR   EMBL; BC020224; AAH20224.1; -; mRNA.
DR   EMBL; AF386792; AAK70871.1; -; Genomic_DNA.
DR   PIR; JU00327; TVHUP1.
DR   PDB; 1XQZ; X-ray; A=14-313.
DR   PDB; 1XR1; X-ray; A=14-313.
DR   PDB; 1XWS; X-ray; A=1-313.
DR   PDB; 1YHS; X-ray; A=33-305.
DR   PDB; 1YI3; X-ray; A=33-305.
DR   PDB; 1YI4; X-ray; A=33-305.
DR   PDB; 1YWV; X-ray; A=1-313.
DR   PDB; 2BIK; X-ray; B=1-313.
DR   PDB; 2BIL; X-ray; B=1-313.
DR   Ensembl; ENSG00000137193; Homo sapiens.
DR   HGNC; HGNC:8986; PIM1.
DR   H-InvDB; HIX0005835; -.
DR   MIM; 164960; -.
DR   GO; GO:0005737; C:cytoplasm; TAS.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR   GO; GO:0007275; P:development; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   3D-structure; ATP-binding; Kinase; Nuclear protein;
KW   Nucleotide-binding; Phosphorylation; Proto-oncogene;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN        38    290       Protein kinase.
FT   NP_BIND       44     52       ATP (By similarity).
FT   ACT_SITE     167    167       Proton acceptor (By similarity).
FT   BINDING       67     67       ATP (By similarity).
FT   CONFLICT      15     16       AP -> RA (in Ref. 2).
SQ   SEQUENCE   313 AA;   35686 MW;   35BA76D3666B69A3 CRC64;
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Query Match           98.1%;   Score 1636;   DB 1;   Length 313;
Best Local Similarity  97.1%;   Pred. No. 7.4e-113;
Matches 304;  Conservative  6;  Mismatches  3;  Indels  0;  Gaps  0;

Qy          1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVIIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVIIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
              |||||||||:||||||||::||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPSPSK 313
              |||||||||| |||
Db        301 EIHLHSLSPSPSK 313
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Db 301 EIHLHSLSPGPSK 313

RESULT 4
Q5T7H7_HUMAN
ID   Q5T7H7_HUMAN PRELIMINARY; PRT; 313 AA.
AC   Q5T7H7;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Pim-1 oncogene (Proviral integration site 1).
GN   Name=PIM1; ORFNames=RP3-355M6.1-003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Laird G.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AL353379; CAI20116.1; -; Genomic_DNA.
DR   SMR; Q5T7H7; 32-308.
DR   Ensembl; ENSG00000137193; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkin.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Serine/threonine-protein kinase.
SQ   SEQUENCE 313 AA; 35686 MW; 35BA76D368B69A3 CRC64;

Query Match   98.1%; Score 1636; DB 2; Length 313;
Best Local Similarity   97.1%; Pred. No. 7.4e-113;
Matches 304; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         |||||||||||||||||| ||||||| ||||||||||||||||||||||||||||||||:|
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy 61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLILDLNRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLILDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQATA 300
         ||||||| : |||| ||||||||||||||||| ||||||| |||||||||||||||||||
Db 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy 301 EIHLHSLSPGPSK 313
         |||||||||||||
Db 301 EIHLHSLSPGPSK 313

RESULT 5
PIM1_BOVIN
ID   PIM1_BOVIN STANDARD; PRT; 313 AA.
AC   Q9N0P9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21109090; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2;
RA   Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;
RT   "cDNA cloning, sequencing and characterization of bovine pim-1.";
RL   Vet. Immunol. Immunopathol. 78:177-195(2001).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AF259078; AAF67200.1; -; mRNA.
DR   HSSP; Q63450; 1A06.
DR   SMR; Q9N0P9; 32-308.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Kinase; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN   38   290   Protein kinase.
FT   NP_BIND   44   52   ATP (By similarity).
FT   ACT_SITE   167   167   Proton acceptor (By similarity).
FT   BINDING   67   67   ATP (By similarity).
SQ   SEQUENCE 313 AA; 35630 MW; 9EF40229A847AD47 CRC64;

Query Match   97.7%; Score 1630; DB 1; Length 313;
Best Local Similarity   97.1%; Pred. No. 2.1e-112;
Matches 304; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCSDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy 61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLILDLNRG 180
         |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHDCGVLHRDIKDENLILDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

RESULT 6

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ID    Q8CFN8_MOUSE PRELIMINARY;     PRT;   313 AA.
AC    Q8CFN8;
DT    01-MAR-2003 (TrEMBLrel. 23, Created)
DT    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT    10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE    Proviral integration site 1.
GN    Name=Pim1;
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC    Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    NUCLEOTIDE SEQUENCE.
RC    STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX    MEDLINE=22238225; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA    Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA    Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA    Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA    Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA    Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA    Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA    Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA    Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA    Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA    Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA    Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA    Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA    Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA    Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA    Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA    Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT    "Generation and initial analysis of more than 15,000 full-length human
RT    and mouse cDNA sequences.";
RL    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN    [2]
RP    NUCLEOTIDE SEQUENCE.
RC    STRAIN=C57BL/6; TISSUE=Brain;
RA    Strausberg R.;
RL    Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN    [3]
RP    NUCLEOTIDE SEQUENCE.
RC    STRAIN=C57BL/6; TISSUE=Eye;
RA    Strausberg R.;
RL    Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN    [4]
RP    NUCLEOTIDE SEQUENCE.
RA    Strausberg R.;
RL    Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC    -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC    -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
DR    EMBL; BC042885; AAH42885.1; -; mRNA.
DR    EMBL; BC053019; AAH53019.1; -; mRNA.
DR    EMBL; BC055316; AAH55316.1; -; mRNA.
DR    SMR; Q8CFN8; 32-308.
DR    Ensembl; ENSMUSG00000024014; Mus musculus.
DR    MGI; MGI:97584; Pim1.
DR    GO; GO:0005524; F:ATP binding; IEA.
DR    GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR    GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR    InterPro; IPR000719; Prot_kinase.
DR    InterPro; IPR008271; Ser_thr_pkin_AS.
DR    InterPro; IPR002290; Ser_thr_pkinase.
DR    Pfam; PF00069; Pkinase; 1.
DR    ProDom; PD000001; Prot_kinase; 1.
DR    SMART; SM00220; S_TKc; 1.
DR    PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR    PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR    PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW    ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW    Serine/threonine-protein kinase.
SQ    SEQUENCE   313 AA;  35451 MW;  1294F16A03B7C7D7 CRC64;
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Query Match             95.3%;
Best Local Similarity   94.6%;
Matches   296;          Conservative
Score 1589;  DB 2;  Length 313;
Pred. No. 2.2e-109;
8;  Mismatches   9;  Indels   0;  Gaps   0;
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Qy      1  MLLSKINSLAHLRRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
           |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MLLSKINSLAHLRAAPCNDLIHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60

Qy     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120

Qy    121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHCNGVLHRDIKDENLILIDLNRG  180
           |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHCNGVLHRDIKDENLILDLSRG  180

Qy    181  ELKLIDFGSGGALLKDTVVTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  EIKLIDFGGSGALLKDTVVTDFDGTRVVYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy    241  PFEHDEEIVRGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQETA  300
           ||||||||||:|:||||:|||||||||||||||||||||||||:|||||||||||||||||
Db    241  PFEHDEEIIKGQVFFRQRVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300

Qy    301  EIHLHSLSPSPSK  313
           ||||||||:||||
Db    301  EIHLHSLSPGPSK  313
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RESULT 7

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ID    PIM1_MOUSE     STANDARD;     PRT;   313 AA.
AC    P06803;
DT    01-JAN-1988 (Rel. 06, Created)
DT    01-JAN-1988 (Rel. 06, Last sequence update)
DT    13-SEP-2005 (Rel. 48, Last annotation update)
DE    Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN    Name=Pim1; Synonyms=Pim-1;
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC    Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    NUCLEOTIDE SEQUENCE.
RX    MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
RA    Selten G., Cuypers H.T., Boelens W., Robanus-Maandag E., Verbeek J.,
RA    Domen J., van Beveren C., Berns A.;
RT    "The primary structure of the putative oncogene pim-1 shows extensive
RT    homology with a protein kinase.";
RL    Cell 46:603-611(1986).
RN    [2]
RP    INTERACTION WITH RP9.
RX    MEDLINE=20389540; PubMed=10931201;
RA    Maita H., Harada Y., Nagakubo D., Kitaura H., Ikeda M., Tamai K.,
RA    Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
RT    "PAP-1, a novel target protein of phosphorylation by Pim-1 kinase.";
RL    Eur. J. Biochem. 267:5168-5178(2000).
CC    -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC    -!- SUBUNIT: Binds to RP9.
CC    -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
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```
Qy    301  EIHLHSLSPSPSK  313
           ||||||||:||||
Db    301  EIHLHSLSPGPSK  313
```

Left column

```
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- DISEASE: Frequently activated by provirus insertion in murine
CC       leukemia virus-induced T-cell lymphomas.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
```

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DR   EMBL; M13945; AAA39930.1; -; Genomic_DNA.
DR   PIR; A24169; TVMSP1.
DR   HSSP; Q63450; 1A06.
DR   SMR; P06803; 32-308.
DR   Ensembl; ENSMUSG00000024014; Mus musculus.
DR   MGI; MGI:97584; Pim1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN       38    290       Protein kinase.
FT   NP_BIND      44     52       ATP (By similarity).
FT   ACT_SITE    167            Proton acceptor (By similarity).
FT   BINDING      67            ATP (By similarity).
SQ   SEQUENCE   313 AA;  35537 MW;  79F4779E9DCBDC16 CRC64;

Query Match             95.0%;  Score 1584;  DB 1;  Length 313;
Best Local Similarity   94.2%;
Matches  295;  Conservative   8;  Mismatches  10;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          ||||||||||||||||:|||||||||||||||||||| ||||||||||||||||||||||
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQVQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGSFSGVIRLLDWFERDPSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |:||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGSFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||:|||:|||||||||||||||||||||||||||:||||:|
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLSRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |:||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATTA 300
          ||||||||:||||:|||:|||||||||:||||||||||||||||:|||||| |:|||||:
Db  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPSPSK 313
          |||||||||:| |
Db  301 EIHLHSLSPGSSK 313

RESULT 8
PIM3_COTJA
ID   PIM3_COTJA     STANDARD;      PRT;   323 AA.
AC   Q9PUB5;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (qpim).
GN   Name=PIM3; Synonyms=PIM-3;
OS   Coturnix coturnix japonica (Japanese quail).
```

Right column

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=93934;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20180111; PubMed=10713710; DOI=10.1038/sj.onc.1203355;
RA   Eichmann A., Yuan L., Breant C., Alitalo K., Koskinen P.J.;
RT   "Developmental expression of Pim kinases suggests functions also
RT   outside of the hematopoietic system.";
RL   Oncogene 19:1215-1224(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
```

```
DR   EMBL; AJ310845; CAB62386.1; -; mRNA.
DR   HSSP; Q63450; 1A06.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       40    291       Protein kinase.
FT   NP_BIND      46     54       ATP (By similarity).
FT   ACT_SITE    168            Proton acceptor (By similarity).
FT   BINDING      69            ATP (By similarity).
SQ   SEQUENCE   323 AA;  36597 MW;  E2A4FA20B6F63996C CRC64;

Query Match             68.2%;  Score 1137;  DB 1;  Length 323;
Best Local Similarity   67.3%;
Matches  212;  Conservative  43;  Mismatches  56;  Indels   4;  Gaps   4;

Qy    1 MLLSKINSLAHL-RAAPCNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIRV 58
          |||||  |||| | |  |  ||  ||||||  |   ||| |||| :|| :||| ||| || :
Db    1 MLLSKFGSLAHICSPASMDHLPVKILPPVVKEKPFDKYYQVGSVLGSSGFGTVYAGSRT 60

Qy   59 ADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGSFSGVIRLLDWFERPDSFVL 118
          || |||| |||| |:| :|| :|   |:|  |:|||||||||  ||| :||||||||||:|
Db   61 ADGLPVAVKHVVKERVTEWGTI-GGVMVPLEIVLLKKVSSGFRGVIKLLDWYERPDGFLI 119

Qy  119 ILERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLN 178
          ::|  | |:||||||||:||| | |||  | |||||||  |  |||| |||  |  | |
Db  120 VMERPELVKDLFDFITEKGALDEDTARGFRQVLEAVRHCICGCGVVHRDIKLDWYERPDGFLI 179

Qy  179 RGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG 238
          |||:||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  120 RGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGILLYDMVCG 239

Qy  239 DIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQ 297
          ::||||:||| :|:||  | : |:|| |:|||:|||||||:||  :|  :|||   |:
Db  240 DIPFEQDEILRGRLYFRRRISPECQQLIKWCLSLRPSDRPTLEQIFDHQWMHKSEVVKS 297

Qy  298 ATAEIHLHSLSPSPS 312
           ::| |||||||| |
Db  300 EDCDIRLRTLDTDVS 314

RESULT 9
PIM3_HUMAN
ID   PIM3_HUMAN     STANDARD;      PRT;   326 AA.
```

AC   Q86V86; Q68BM2;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=PIM3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY.
RC   TISSUE=Liver;
RX   PubMed=15540201; DOI=10.1002/ijc.20719;
RA   Fujii C., Nakamoto Y., Lu P., Tsuneyama K., Popivanova B.K.,
RA   Kaneko S., Mukaida N.;
RT   "Aberrant expression of serine/threonine kinase Pim-3 in
RT   hepatocellular carcinoma development and its role in the proliferation
RT   of human hepatoma cell lines.";
RL   Int. J. Cancer 114:209-218(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
CC   -!- FUNCTION: May be involved in cell cycle progression and anti-
CC   apoptosis process. Implicated in proliferation of human hepatoma
CC   cell lines.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- TISSUE SPECIFICITY: Widely expressed. No expression in colon,
CC   thymus, and small intestine. Expressed in human hepatoma cell
CC   lines but not in normal liver tissues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
DR   EMBL; AB111795; BAD42438.1; -; mRNA.
DR   EMBL; BC050239; -; NOT_ANNOTATED_CDS; mRNA.
DR   Ensembl; ENSG00000198355; Homo sapiens.
DR   HGNC; HGNC:19310; PIM3.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pKin_AS.

DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   40   293   Protein kinase.
FT   NP_BIND   46   54   ATP (By similarity).
FT   ACT_SITE   170   170   Proton acceptor (By similarity).
FT   BINDING   69   69   ATP (By similarity).
SQ   SEQUENCE   326 AA;   35863 MW; 41FDF9DD24673A162 CRC64;

Query Match
Best Local Similarity   69.6%;
Matches 220; Conservative 34; Mismatches 52; Indels 10; Gaps 7;

Score 1135; DB 1; Length 326;
Pred. No. 8.7e-76;

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Qy    1  MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGGSGFGSVYSGIR  57
         |||||:..||||       :..| .| |:  ||:|||:||||..||.|||||.|.|.|.|
Db    1  MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYAGSR  59

Qy   58  VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
         :|| ||||:|||.|.|::.||.| .| ||||:||||.||    ||:.|||||||||||| 
Db   60  IADGLPVAVKHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy  116  FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
         |.|:||||||.|||||||||||||.|.||| ||.|||.||||||.||:|||||||||:|:
Db  119  FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV 178

Qy  176  DLNRGELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM  235
         ||..||||||||||||||||||.||||||||||||||||||||||||:.|||||:|||| 
Db  179  DLRSGELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM  238

Qy  236  VCGDIPFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWM--QDV 293
         ||||||||.|||:..|.: ||.||| ||| |||||||||||.:||| .:| .||||   | 
Db  239  VCGDIPFEQDEEILRGRLLFRRRVSPECCQLIRWCLSLRPSERPSLDQIAAHPWMLGADG  298

Qy  294  LLPQATAEIHLHSLSP 309
         ..|: :||:|:|.| | 
Db  299  GAPE-SCDLRLCTLDP 313
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RESULT 10
PIM3_MOUSE
ID   PIM3_MOUSE   STANDARD;   PRT;   326 AA.
AC   P58750;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=Pim3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!-
RN [1]
RP NUCLEOTIDE SEQUENCE.
CC -!-
RC SIMILARITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC --
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC --
DR EMBL; BC017621; AAH17621.1; -; mRNA.
DR EMBL; BC026639; AAH26639.1; -; mRNA.
DR HSSP; Q03656; 1HOW.
DR Ensembl; ENSMUSG00000035828; Mus musculus.
DR MGI; MGI:1355297; Pim3.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser/thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation; Transferase.
KW Serine/threonine-protein kinase.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
FT DOMAIN   40   293   Protein kinase.
FT NP_BIND   46   54   ATP (By similarity).
FT ACT_SITE   170   Proton acceptor (By similarity).
FT BINDING   69   69   ATP (By similarity).
SQ SEQUENCE   326 AA; 35970 MW; DD68CBF46354851E CRC64;

Query Match   67.9%; Score 1132.5; DB 1; Length 326;
Best Local Similarity   72.5%; Pred. No. 1.3e-75;
Matches   214; Conservative   30; Mismatches   44; Indels   7; Gaps   5;

Qy   1 MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR 57
          ||||||||| | ||| ||||||||||||| |||||||||||||||||||||||||||
Db   1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR 59

Qy   58 VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
          :|:||:|||||||||:|||||:||||||||:|||||||| :|||:|||||||||||||
Db   60 IADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFERDG 118

Qy   116 FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db   119 FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV 178

Qy   176 DLNRGELKLIDFGSGALLKDTVVTDFDGTRVSPPEWIRYHRYHGRSAAVWSLGILILYDM 235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 DLRSGELKLIDFGSGAVLKDTVVTDFDGTRVSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy   236 VCGDIPFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWM 290
          |||||||| |:| |||||||||||||||||||||||||||||||||||||||||||
Db   239 VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM 293

GN Name=Pim3; Synonyms=Kid1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RA Konietzko U., Kuhl D.;
RT "KID-1, a protein kinase induced by depolarization in brain.";
RL J. Biol. Chem. 273:16535-15543(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=98298176; PubMed=9632723; DOI=10.1074/jbc.273.26.16535;
RA Feldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L.,
RA Bazan N.G., Baudry M., Herschman H.R.;
RT "KID-1, a protein kinase induced by depolarization in brain.";
RL J. Biol. Chem. 273:16535-15543(1998).
CC -!- FUNCTION: Protein serine/threonine kinase activity; IDA.
CC -!- SUBMITTED (AUG-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- "Pim-3 is a member of the pim kinase family.";
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- TISSUE SPECIFICITY: Present in a number of unstimulated tissues,
CC   including brain.
CC -!- INDUCTION: By membrane depolarization or forskolin.
CC -!- PTM: Autophosphorylated.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC --
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC --
DR EMBL; AF086224; AAC68900.1; ALT_INIT; mRNA.
DR EMBL; AF057026; AAC36055.1; -; mRNA.
DR HSSP; Q03656; 1HOW.
DR RGD; 620462; Pim3.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser/thr_pkinase.
KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation; Transferase.
KW Serine/threonine-protein kinase.
GO GO:0004674; F:protein serine/threonine kinase activity; IDA.
GO GO:0046777; P:autophosphorylation; IDA.
GO GO:0016572; P:histone phosphorylation; IDA.
FT DOMAIN   40   293   Protein kinase.
FT NP_BIND   46   54   ATP (By similarity).
FT ACT_SITE   170   Proton acceptor (By similarity).
FT BINDING   69   69   ATP (By similarity).
SQ SEQUENCE   326 AA; 36002 MW; DD6C9BF4635F851E CRC64;

Query Match   67.8%; Score 1131.5; DB 1; Length 326;
Best Local Similarity   72.5%; Pred. No. 1.6e-75;
Matches   214; Conservative   30; Mismatches   44; Indels   7; Gaps   5;

Qy   1 MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR 57
          ||||||||| | ||| ||||||||||||| |||||||||||||||||||||||||||
Db   1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR 59

Qy   58 VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
          :|:||:|||||||||:|||||:||||||||:|||||||| :|||:|||||||||||||
Db   60 IADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy   116 FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
          ||||||||||||||||||||||||| :|||:|||||:||||||||||||||||||||||
Db   119 FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV 178

RESULT 11
ID   PIM3_RAT   STANDARD;   PRT;   326 AA.
AC   O70444;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Protein kinase
DE   Kid-1) (Kinase induced by depolarization).

RESULT 12

```
Qy   176  DLNRGELKLIDFGSGGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM  235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179  DLRSGELKLIDFGSGAVLKDTVTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM  238

Qy   236  VCGDIPFEHDEEIVKGQVYFRQVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM  290
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   239  VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM  293
```

Query Match   67.8%; Score 1131.5; DB 2; Length 380;
Best Local Similarity   72.5%; Pred. No. 1.9e-75;
Matches 214; Conservative 30; Mismatches 44; Indels 7; Gaps 5;

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Qy   236  VCGDIPFEHDEEIVKGQVYFRQVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM  290
Db   293  VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM  347
```

RESULT 13

```
Qy     1  MLLSKINSLAHLRAAP--CNDLIHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR   57
          |:|:||||||||||:||  ::||:||:||||:|  :|||||:||:|||||||||||:||||
Db     1  MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQGAVLGSGGFGTVYAGSR   57

Qy    58  VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS  115
          ||||||||||||:|||:|||||||||||||||||||||:  ||||:|||||||||||||
Db    55  MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQGAVLGSGGFGTVYAGSR  113

Qy   116  FLVLERFBPPVQDLFDFITERGALDEPLARRFFAQVLAAVRHCHCNCGVVHRDIKDENLLV  175
          ||||||:||:||||||||||||||||||||||:|||||:|||||||||||||||||||:|
Db   114  IADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG  172

Qy   176  DLNRGELKLIDFGSGGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM  235
          ||||||||||||||||||||||||||||||||||||||||||||||||||:|||:||||
Db   173  FLVLERFBPPVQDLFDFITERGALQEELARSFWQVLEAVRHCHCNCGVVHRDIKDENLLV  232

Qy   236  VCGDIPFEHDEEIVKGQVYFRQVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM  290
Db   233  DLRSGELKLIDFGSGAVLKDTVTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM  292
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Query Match   67.1%; Score 1119; DB 2; Length 325;
Best Local Similarity   72.2%; Pred. No. 1.3e-74;
Matches 213; Conservative 31; Mismatches 43; Indels 8; Gaps 6;

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Qy     1  MLLSKINSLAHLRAAP--CNDLIHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR   57
Db     1  MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQGAVLGSGGFGTVYAGSR   59

Qy    58  VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS  115
Db    60  IADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG  118

Qy   116  FVILERFBPPVQDLFDFITERGALDEPLARRFFAQVLAAVRHCHCNCGVVHRDIKDENLLV  175
Db   119  FLVLERFBPPVQDLFDFITERGALQEELARSFWQVLEAVRHCHCNCGVVHRDIKDENLLV  178
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Qy   176 DLNRGELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
          || |||||||||||||||||||||||||||||||||:|| |||||||||||||::|||||
Db   179 DLRSGELKLIDFGSGAVLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy   236 VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM 290
          ||||||||| ||:||| |||||| |||||||||||||| ||||| |||||:|| |
Db   239 VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDKL-CHPWM 292

RESULT 14

Qy   3 LSKINSLAHLRAAPCNDLLHANKLAPGKE------KEPLESQYQVGPLLGSSGGFGSVYR 58
          |:||| || | |:|| | || || | | ||:||:|||| ||||||||||
Db   1 MSSVQVIYHQK--IHNYLNSVPFKDDLPAVKEPPENCYQVGPVVIGTGGFGTVYSGIRV 57

Qy   59 ADNLPVAIKHIVEKDRISDWGELENGTRVPMEVVLLKKVSSGFGSGVIRLLDWFERPDSFVL 118
          ||||| |:|| |:||:|| ||||:|||| || | :| ||||:| |||| |||:|:| ||||
Db   58 SDKLPVAIKHVSRDRIGEMKHM-NGTLVPLEIYLLKKVSNGCRGVIRLLDWYERPDGFII 116

Qy   119 ILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLN 178
          :|| |||||||||||||||||:|||| |:||||||||||:|| |||||||||||||||||
Db   117 IMRPEPVQDLFDFITERGALGEELATNFPRQVVEAVRHCHSCDVVHRDIKDENILVDLR 176

Qy   179 RGELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG 238
          |||||||||||||||||||| |||||||||||||||||||||||| |||||||||||||
Db   177 TAELKLIDFGSGALLRDAVTDFDGTRVYSPPEWIRFHXYHGRSATVWSLGILLYDMVCG 236

Qy   239 DIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM-QDVLL 295
          ||||| ||:| |::| | |||| ||:|| |||||||| ||:| | |:|| | ||||
Db   237 DIPFEHDDEILKGHKIQYRCRVSRECQHLIEWCLSKRPSDRPPSLEQILAPPWMSQDNFL 294

Db   1 MSSVQVIYHQK---IHNYLNSVFPKDDLPAVKEPFENCYQVGPVIIGTGGFGTVYSGIRV 57

Query Match   66.6%;   Score 1110.5;   DB 2;   Length 318;
Best Local Similarity   68.8%;   Pred. No. 5.5e-74;
Matches 205; Conservative 40; Mismatches 44; Indels 9; Gaps 4;

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KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN        40    291   Protein kinase.
FT   NP_BIND       46     54   ATP (By similarity).
FT   ACT_SITE     168    168   Proton acceptor (By similarity).
FT   BINDING       69     69   ATP (By similarity).
FT   MOD_RES        4      4   Phosphoserine (by similarity)
FT                             (partial).
FT   MOD_RES      190    190   Phosphoserine (by autocatalysis).
FT   MOD_RES      205    205   Phosphothreonine (by autocatalysis)
FT                             (partial).
SQ   SEQUENCE    323 AA;  36964 MW;  AB4DDG1E7A99A38F CRC64;

Query Match          66.1%;     Score 1102.5;  DB 1;  Length 323;
Best Local Similarity  68.6%;     Pred. No. 2.2e-73;
Matches  203; Conservative  40; Mismatches  42; Indels  11; Gaps  4;

Qy     1 MLLSKINSLAHLRAAPCN-------DLHANKLAPGK-EKEPLESQYQVGPLLGSSGFGSVYS    54
         |||||    |||||    |         |||||||||: :: |||:|||||||||||||
Db     1 MLLSKFGSLAHI---------CNPSNMEHLPVKILQPVVDKEPPEKVYQVGSVVASGGFGTVYS    56

Qy    55 GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPVMEVVLLKKVSSGFSGVIRLLDWFERPD   114
         |:|||  ||||| | || |||:|||||||| | |  |||| :||||||| |  ||||:||
Db    57 DSRIADGQPVAVKHVAKERVTEWGTL-NGVMVPLEIVLLKKVPTAFRGVINLLDWYERPD    115

Qy   115 SFVLILERPEPVQDLFDFITERGALQELARSFFWQVLEAVRHCHNCGVLHRDIKDENIL    174
         :|:::||||||||||||: :: ||||||||:|||||::||||||:|||||||||||:
Db   115 AFLIVMERPEPVKDLFDYITEKGPLDEDTARGFFRQVLEAVRHCYNCGVVHRDIKDENLL   175

Qy   175 IDLNRGELKLIDFGSGALLKDTVYTDFDGTRVVSPPEWIRYHRYHGRSAAVWSLGILLYD   234
         :| ||||||||||||||||||||||||:||||||||||||||||||||| |||||||||
Db   176 VDTRNGELKLIDFGSGALLKDTVYTDFDGTRVVSPPEWVRYHRYHGRSATVWSLGVLLYD   235

Qy   235 MVCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM     290
         ||||||||| ||||||||||| :: ::|||: |||||||||||||||||: :|:|||||
Db   236 MVYGDIPFEQDEEIVRVRLCFRRRISTECQQLIKWCLSLRPSDRPTLEQIFDHPWM    291
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Search completed: May 4, 2006, 05:18:59
Job time : 123 secs

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OM protein - protein search using sw model

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GenCore version 5.1.7

Run on: May 4, 2006, 05:25:14 ; Search time 28.6667 Seconds
                                             (without alignments)
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Title: US-10-705-757-6
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRARPCNDL...........LLPQAASEIHLHSLSPGSSK 313

Scoring table: BLOSUM62
                     Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
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                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/pCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	DB ID	Description
1	1668	100.0	313	2	US-09-237-543-7	Sequence 7, Appl
2	1668	100.0	313	2	US-09-644-450-7	Sequence 7, Appli
3	1584	95.0	313	2	US-09-237-543-8	Sequence 8, Appli
4	1584	95.0	313	2	US-09-644-450-8	Sequence 8, Appli
5	1582	94.8	313	2	US-09-237-543-9	Sequence 9, Appli
6	1582	94.8	313	2	US-09-644-450-9	Sequence 9, Appli
7	1580	94.7	313	1	US-08-463-081B-26	Sequence 26, Appli
8	1580	94.7	313	1	US-08-461-379A-26	Sequence 26, Appli
9	1580	94.7	313	1	US-08-462-390B-26	Sequence 26, Appli
10	1580	94.7	313	1	US-08-462-074E-26	Sequence 26, Appli
11	1580	94.7	313	1	US-08-465-585C-26	Sequence 26, Appli
12	1580	94.7	313	2	US-08-652-446-26	Sequence 26, Appli
13	1355.5	81.3	257	1	US-07-857-224B-41	Sequence 41, Appl
14	1122.5	67.3	455	2	US-09-237-543-5	Sequence 5, Appli
15	1122.5	67.3	455	2	US-09-644-450-5	Sequence 5, Appli
16	1119	67.1	326	2	US-09-237-543-2	Sequence 2, Appli
17	1119	67.1	326	2	US-09-644-450-2	Sequence 2, Appli
18	1113	66.7	323	2	US-09-237-543-6	Sequence 6, Appli
19	1113	66.7	323	2	US-09-644-450-6	Sequence 6, Appli
20	1065.5	63.9	254	2	US-09-237-543-4	Sequence 4, Appli
21	1065.5	63.9	254	2	US-09-644-450-4	Sequence 4, Appli
22	850	51.0	311	2	US-10-184-563-2	Sequence 2, Appli
23	850	51.0	372	2	US-09-949-016-7140	Sequence 7140, Ap
24	379	22.7	1101	2	US-09-770-170-8	Sequence 8, Appli
25	377.5	22.6	776	2	US-09-523-849-34	Sequence 34, Appl
26	373.5	22.4	256	2	US-09-964-956-74	Sequence 74, Appl
27	372	22.3	1356	2	US-09-770-170-6	Sequence 6, Appli
28	371.5	22.3	256	2	US-09-964-956-72	Sequence 72, Appl
29	371	22.2	778	2	US-10-116-326-2	Sequence 2, Appli
30	371	22.2	778	2	US-10-003-690-2	Sequence 2, Appli
31	371	22.2	778	2	US-10-803-277-2	Sequence 2, Appli
32	367.5	22.0	1323	2	US-09-633-328B-4	Sequence 4, Appli
33	367	22.0	512	2	US-09-770-170-2	Sequence 2, Appli
34	367	22.0	512	2	US-09-633-328B-2	Sequence 2, Appli
35	361.5	21.7	281	2	US-09-248-796A-20512	Sequence 20512, A
36	361.5	21.7	630	2	US-10-355-975A-38	Sequence 38, Appl
37	359.5	21.6	631	2	US-10-355-975A-11	Sequence 11, Appl
38	359.5	21.6	631	2	US-09-930-181-2	Sequence 2, Appli
39	349.5	21.0	668	2	US-09-355-664B-11	Sequence 11, Appl
40	349.5	21.0	668	2	US-10-054-579-2	Sequence 2, Appli
41	349.5	21.0	674	2	US-10-283-328A-2	Sequence 2, Appli
42	345.5	20.7	674	2	US-10-283-247-2	Sequence 2, Appli
43	345.5	20.7	674	2	US-10-283-247-7	Sequence 7, Appli
44	345	20.7	722	2	US-10-283-247-8	Sequence 8, Appli
45	344	20.6	722	2	US-08-817-832B-32	Sequence 32, Appli

ALIGNMENTS

RESULT 1
US-09-237-543-7

; Sequence 7, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 03580U/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-237-543-7

Query Match   100.0%; Score 1668; DB 2; Length 313;
Best Local Similarity   100.0%;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDPFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDPFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
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Db   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVVSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EIKLIDFGSGALLKDTVYTDFDGTRVVSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy   301 EIHLHSLSPGSSK 313
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Db   301 EIHLHSLSPGSSK 313

RESULT 2
US-09-644-450-7

; Sequence 7, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-644-450-7

Query Match   100.0%;   Score 1668;   DB 2;   Length 313;
Best Local Similarity   100.0%;   Pred. No. 9e-162;
Matches 313;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
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Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
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Db  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGSSK 313
         |||||||||||||
Db  301 EIHLHSLSPGSSK 313
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RESULT 3
US-09-237-543-8
; Sequence 8, Application US/0923754 3A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-8

Query Match   95.0%;   Score 1584;   DB 2;   Length 313;
Best Local Similarity   94.2%;   Pred. No. 3.4e-153;
Matches 295;   Conservative   8;   Mismatches   10;   Indels   0;   Gaps   0;

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         ||:||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRRAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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RESULT 4
US-09-644-450-8
; Sequence 8, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-644-450-8

Query Match   95.0%;   Score 1584;   DB 2;   Length 313;
Best Local Similarity   94.2%;   Pred. No. 3.4e-153;
Matches 295;   Conservative   8;   Mismatches   10;   Indels   0;   Gaps   0;

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Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         ||:||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
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Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         ||||||||||||||||||||||||:||||||||||||||||||||||||||||||||:|||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         |||||||||:||||||||||||||||||||||||||||||||||:|||||||||||:| :
Db  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPSPSK 313
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RESULT 5
US-09-237-543-9
; Sequence 9, Application US/0923754 3A
; Patent No. 6143540

; GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/237,543A
;   CURRENT FILING DATE: 1999-01-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: Patentin Ver. 2.0
;
;   SEQ ID NO 9
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-237-543-9

Qy Query Match   94.8%; Score 1582; DB 2; Length 313;
;   Best Local Similarity   93.9%; Pred. No. 5.4e-153;
    Matches 294; Conservative   10; Mismatches   9; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db   1 MLLSKINSLAHLRRAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||.||
Db 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 EIKLIDFGSGALLKDTVYTDFDGTRVSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIKGQVFFRQVTVSSECQHLIIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         ||:||||||.|||||||||||||||:|||||||:||||||||||||||||:|||||: |
Db 241 PFEHDEEIIRGQVFFRQVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSSK 313
         ||||||||||||||
Db 301 EIHLHSLSPGPSK 313

RESULT 6
US-09-644-450-9
;   Sequence 9, Application US/09644450
;   Patent No. 6383791
; GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/644,450
;   CURRENT FILING DATE: 2000-08-23
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: Patentin Ver. 2.0
;
;   SEQ ID NO 9
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-644-450-9

Qy Query Match   94.8%; Score 1582; DB 2; Length 313;
;   Best Local Similarity   93.9%; Pred. No. 5.4e-153;
    Matches 294; Conservative   10; Mismatches   9; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db   1 MLLSKINSLAHLRRAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

RESULT 7
US-08-463-081B-26
;   Sequence 26, Application US/08463081B
;   Patent No. 5871960 5837487
; GENERAL INFORMATION:
;   APPLICANT: Smith, Kendall A. & Beadling, Carol
;   TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
;   TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
;   NUMBER OF SEQUENCES: 35
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
;   STREET: 444 South Flower St. - Suite 1900
;   CITY: Los Angeles
;   STATE: California
;   COUNTRY: USA
;   ZIP: 90071
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0,
;   SOFTWARE: Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/463,081B
;   FILING DATE: 5-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/104,736
;   FILING DATE: 10-AUG-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/796,066
;   FILING DATE: 20-NOV-91
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Viviana Amzel, Ph. D.
;   REGISTRATION NUMBER: 30,930
;   REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (213) 622-7700
;   TELEFAX: (213) 489-4210
;   INFORMATION FOR SEQ ID NO: 26:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 313 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: n.a.
;   TOPOLOGY: n.a.
;   MOLECULE TYPE: peptide
US-08-463-081B-26

Qy Query Match   94.7%; Score 1580; DB 1; Length 313;
;   Best Local Similarity   93.9%; Pred. No. 8.6e-153;
    Matches 294; Conservative   10; Mismatches   9; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||

RESULT 8
US-08-461-379A-26
; Sequence 26, Application US/0846137A
; Patent No. 5871961
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide, Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; ADDRESSEE: (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,379A
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108; 08/104,736
; APPLICATION NUMBER: & 07/796,066
; FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: DART-070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)470-0700
; TELEFAX: (610)470-0701
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
US-08-461-379A-26
; MOLECULE TYPE: peptide

Query Match 94.7%; Score 1580; DB 1; Length 313;
Best Local Similarity 93.9%; Pred. No 8.6e-153;
Matches 294; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

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Qy   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
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Db   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 EIKLIDFGSGALLKDTVYTDFPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS 300
         ||||||||:|||||||| ||||||||:|||:|||||||:||||:|||||||:| ||||:|
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy 301 EIHLHSLSPGSSK 313
         |||||||||| ||
Db 301 EIHLHSLSPGPSK 313
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RESULT 9
US-08-462-390B-26
; Sequence 26, Application US/0846239B
; Patent No. 5882894
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A.; & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; ADDRESSEE: (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,390B
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: USSN 08/104,736
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: USSN 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: DART-040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)407-0700
; TELEFAX: (610)407-0701
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
US-08-462-390B-26
; MOLECULE TYPE: peptide

Query Match 94.7%; Score 1580; DB 1; Length 313;

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Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
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Db   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 EIKLIDFGSGALLKDTVYTDFPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS 300
         ||||||||:|||||||| ||||||||:|||:|||||||:||||:|||||||:| ||||:|
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
         |||||||||||||
Db 301 EIHLHSLSPGPSK 313
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Best Local Similarity 93.9%; Pred. No. 8 6e-153; Mismatches 9; Indels 0; Gaps 0;
Matches 294; Conservative 10;

```
Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD  60
Db    1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVSD  60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
Db  181 ELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGSSK 313
Db  301 EIHLHSLSPGPSK 313
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Query Match 94.7%; Score 1580; DB 2; Length 313;
Best Local Similarity 93.9%; Pred. No. 8 6e-153; Mismatches 9; Indels 0; Gaps 0;
Matches 294; Conservative 10;

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Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD  60
Db    1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVSD  60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
Db  181 ELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGSSK 313
Db  301 EIHLHSLSPGPSK 313
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;   TOPOLOGY: n.a.
;   MOLECULE TYPE: peptide
US-08-465-585C-26

Query Match   94.7%; Score 1580; DB 2; Length 313;
Best Local Similarity   93.9%; Pred. No. 8.6e-153;
Matches 294; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

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Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFPGSVYSGIRVAD 60
        ||||||||||||||| |||||||||||||||||||||||||||||| |||||||||||:|
Db    1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
        ||||||||||||||||||||||:|||:|||||||||||||||||||||||||||||||:||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240
        |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
        |||||||||:||||||||:||||||||:||||:|||||||:||||:||||||::|||::|:
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSSK 313
        ||||||||||||:|
Db  301 EIHLHSLSPGPSK 313
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RESULT 12
US-08-652-446-26
Sequence 26, Application US/08652446
Patent No. 6057427
GENERAL INFORMATION:
;   APPLICANT: Smith, Kendall A. & Beadling, Carol
;   TITLE OF INVENTION: Nucleic Acids Encoding CR5
;   TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
;   TITLE OF INVENTION: Expression Thereof
;   NUMBER OF SEQUENCES: 38
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
;   ADDRESSEE: (B) STREET: 444 South Flower St. - Suite 1900
;   CITY: Los Angeles
;   STATE: California
;   COUNTRY: USA
;   ZIP: 90071
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0,
;   SOFTWARE: Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08,652,446
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EP App. # 96921319.8
;   FILING DATE: 5-JAN-1998
;   APPLICATION NUMBER: PCT/US/96/09194
;   FILING DATE: 5-JUN-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/330,108
;   FILING DATE: 27-OCT-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/463,074
;   FILING DATE: 5-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/462,337
;   FILING DATE: 5-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/462,390
;   FILING DATE: 5-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/465,585
;   FILING DATE: 5-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/461,379
;   FILING DATE: 5-JUN-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/739,523
;   FILING DATE: 29-OCT-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/463,081
;   FILING DATE: 5-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Viviana Amzel, Ph. D.
;   REGISTRATION NUMBER: 30,930
;   REFERENCE/DOCKET NUMBER: FP66 40035
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (213) 622-7700
;   TELEFAX: (213) 489-4210
;   INFORMATION FOR SEQ ID NO: 26:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 313 amino acids
;   TYPE: peptide
;   STRANDEDNESS: n.a.
;   TOPOLOGY: n.a.
;   MOLECULE TYPE: peptide
US-08-652-446-26

Query Match   94.7%; Score 1580; DB 2; Length 313;
Best Local Similarity   93.9%; Pred. No. 8.6e-153;
Matches 294; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

```
Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFPGSVYSGIRVAD 60
        ||||||||||||||| |||||||||||||||||||||||||||||| |||||||||||:|
Db    1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
        ||||||||||||||||||||||:|||:|||||||||||||||||||||||||||||||:||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240
        |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
        |||||||||:||||||||:||||||||:||||:|||||||:||||:||||||::|||::|:
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSSK 313
        ||||||||||||:|
Db  301 EIHLHSLSPGPSK 313
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RESULT 13
US-07-857-224B-41
Sequence 41, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
;   APPLICANT: Benner, Steven A.
;   TITLE OF INVENTION: Predicting Folded Structures of Proteins
;   NUMBER OF SEQUENCES: 114
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Steven A. Benner
;   STREET: Hadlaubstrasse 151
;   CITY: Zurich
;   STATE: none

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COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (international) 41 1 632 2830
TELEFAX: (international) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: rat
FEATURE: Protein kinase; Table 8 Column 46
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
DATE: 1988
US-07-857-224B-41
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Query Match          81.3%;   Score 1355.5;  DB 1;  Length 257;
Best Local Similarity 98.8%;  Pred. No. 5.2e-130;
Matches 256;  Conservative 0;  Mismatches 0;  Indels 3;  Gaps 2;

Qy  36 SQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKK 95
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Db   1 SQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGE--NGTRVPMEVVLLKK 58

Qy  96 VSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAV 155
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Db 239 PSDRPSFEEIRNHPWMQGD 257
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RESULT 14
US-09-237-543-5
Sequence 5, Application US/09237543A
Patent No. 6143540
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
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CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 455
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-237-543-5
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Query Match          67.3%;   Score 1122.5;  DB 2;  Length 455;
Best Local Similarity 71.0%;  Pred. No. 7.1e-106;
Matches 213;  Conservative 31;  Mismatches 43;  Indels 13;  Gaps 5;

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RESULT 15
US-09-644-450-5
Sequence 5, Application US/09644450
Patent No. 6383791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 455
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-644-450-5
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Query Match          67.3%;   Score 1122.5;  DB 2;  Length 455;
Best Local Similarity 71.0%;  Pred. No. 7.1e-106;
Matches 213;  Conservative 31;  Mismatches 43;  Indels 13;  Gaps 5;

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Qy 173 ILIDLSRGEIKLIDFGSGALLKDTVYTDFPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL 232
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Search completed: May 4, 2006, 05:27:22
Job time : 29.6667 secs

GenCore version 5.1.7

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2006, 05:26:13 ; Search time 92.6667 Seconds
                 (without alignments)
                 1411.301 Million cell updates/sec

Post-processing: Minimum Match 0%
                 Maximum Match 10%
                 Listing first 45 summaries

Database :   Published Applications AA Main:*
                 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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                 7: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Scoring: 1 MLLSKINSLAHLRARPCNDL.........LLPQAASEIHLHSLSPGSSK 313

Sequence: 1 MLLSKINSLAHLRARPCNDL.........LLPQAASEIHLHSLSPGSSK 313
Perfect score: 1668
Title: US-10-705-757-6

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1668	100.0	313	3	US-09-971-791-7	Sequence 7, Appli
2	1668	100.0	313	4	US-10-348-081-14	Sequence 14, Appl
3	1668	100.0	313	4	US-10-664-421-2	Sequence 2, Appli
4	1668	100.0	313	4	US-10-705-757-6	Sequence 6, Appli
5	1668	100.0	313	5	US-10-377-268-10	Sequence 10, Appl
6	1668	100.0	313	5	US-10-941-635-2	Sequence 2, Appli
7	1584	100.0	313	3	US-09-971-791-8	Sequence 8, Appli
8	1584	95.0	313	4	US-10-348-081-12	Sequence 12, Appl
9	1584	95.0	313	4	US-10-705-757-4	Sequence 4, Appli
10	1584	94.8	313	3	US-09-971-791-9	Sequence 9, Appli
11	1582	94.8	313	4	US-10-081-119-18	Sequence 18, Appl
12	1582	94.8	313	4	US-10-394-322A-52	Sequence 52, Appl
13	1582	94.8	313	4	US-10-348-081-13	Sequence 13, Appl
14	1582	94.8	313	4	US-10-664-421-1	Sequence 1, Appl
15	1582	94.8	313	4	US-10-664-421-150	Sequence 150, App
16	1582	94.8	313	4	US-10-705-757-2	Sequence 2, Appli
17	1582	94.8	313	5	US-10-377-268-9	Sequence 9, Appli
18	1582	94.8	313	5	US-10-951-388-18	Sequence 18, Appl
19	1582	94.8	313	5	US-10-951-406-18	Sequence 18, Appl
20	1582	94.8	313	5	US-10-951-477-18	Sequence 18, Appl
21	1582	94.8	313	5	US-10-977-087-18	Sequence 18, Appl
22	1582	94.8	313	5	US-10-941-635-1	Sequence 1, Appli
23	1582	94.8	313	5	US-10-941-635-152	Sequence 152, App
24	1580	94.7	313	4	US-10-620-052A-22	Sequence 22, Appl
25	1315	78.8	253	4	US-10-620-052A-71	Sequence 71, Appl
26	1131	67.8	323	4	US-10-664-421-7	Sequence 7, Appli
27	1131	67.8	323	4	US-10-377-268-15	Sequence 15, Appl
28	1131	67.8	323	5	US-10-941-635-7	Sequence 7, Appli
29	1123.5	67.4	326	4	US-10-348-081-6	Sequence 6, App
30	1123.5	67.4	326	4	US-10-705-757-11	Sequence 11, Appl
31	1123.5	67.4	326	5	US-10-377-268-14	Sequence 14, Appl
32	1123.5	67.4	326	6	US-10-941-635-6	Sequence 6, Appli
33	1123.5	67.3	326	4	US-10-348-081-10	Sequence 10, Appl
34	1122.5	67.3	326	4	US-10-705-757-9	Sequence 9, Appli
35	1122.5	67.3	455	3	US-09-971-791-5	Sequence 5, Appli
36	1122.5	67.1	455	3	US-09-971-791-2	Sequence 2, Appli
37	1119	67.1	326	4	US-10-348-081-2	Sequence 2, Appli
38	1119	67.1	326	4	US-10-664-421-166	Sequence 166, App
39	1119	67.1	374	4	US-10-618-941-82	Sequence 82, Appl
40	1119	67.1	374	4	US-10-425-114-54264	Sequence 54264, A
41	1119	67.1	323	4	US-10-425-114-54275	Sequence 54275, A
42	1113	66.7	323	3	US-09-971-791-6	Sequence 6, Appli
43	1113	66.7	323	4	US-10-348-081-11	Sequence 11, Appl
44	1113	66.7	323	4	US-10-664-421-8	Sequence 8, Appli
45	1113	66.7	323	4	US-10-377-268-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-971-791-7

; Sequence 7, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US/09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-971-791-7

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Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
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Qy   181 EIKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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RESULT 2
US-10-348-081-14
; Sequence 14, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: MUELLER, Guenter
; APPLICANT: KORN, Marcus
; APPLICANT: SCHNEIDER, Rudolf
; APPLICANT: TSCHANK, Georg
; TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: DEAV2002/0004 US NP
; CURRENT APPLICATION NUMBER: US/10/348,081
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 14
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-348-081-14

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  Best Local Similarity   100.0%; Pred. No. 8.1e-142;
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Qy 181 EIKLIDFGSGALLKDTVVTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
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Qy 301 EIHLHSLSPGSSK 313
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RESULT 3
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; Sequence 2, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 3.2
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; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-664-421-2

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  Best Local Similarity   100.0%; Pred. No. 8.1e-142;
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; Sequence 6, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
; APPLICANT: GRUENENTHAL GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCE: 029310.5281BUS
; CURRENT APPLICATION NUMBER: US/10/705,757
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
;

; SEQ ID NO 6
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-705-757-6

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Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
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Qy 181 EIKLIDFGSGALLKDTVVTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
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Qy 301 EIHLHSLSPGSSK 313
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RESULT 5
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; Sequence 10, Application US/10377268
; Publication No. US20040171062A1
; GENERAL INFORMATION:
; APPLICANT: HIRTH, KLAUS-PETER
; APPLICANT: MILBURN, MICHAEL VANCE
; TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
; FILE REFERENCE: 039363/0303
; CURRENT APPLICATION NUMBER: US/10/377,268
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: 60/437,929
; PRIOR FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/360,651
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-377-268-10

Query Match   100.0%; Score 1668; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 8.1e-142;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db   1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
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Db 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIKGQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIKGQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy 301 EIHLHSLSPGSSK 313
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Db 301 EIHLHSLSPGSSK 313

RESULT 6
US-10-941-635-2
; Sequence 2, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-941-635-2

Query Match   100.0%; Score 1668; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 8.1e-142;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db   1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIKGQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIKGQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy 301 EIHLHSLSPGSSK 313
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Db 301 EIHLHSLSPGSSK 313

RESULT 7
US-09-971-791-8
; Sequence 8, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-971-791-8

Query Match   100.0%; Score 1668; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 8.1e-142;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db   1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
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Db 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIKGQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIKGQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy 301 EIHLHSLSPGSSK 313
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Db 301 EIHLHSLSPGSSK 313

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Db  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPSPSK 313
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RESULT 8
US-10-348-081-12
Sequence 12, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
;   APPLICANT: KORN, Marcus
;   APPLICANT: MUELLER, Guenter
;   APPLICANT: SCHNEIDER, Rudolf
;   APPLICANT: TSCHANK, Georg
;   TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
;   FILE REFERENCE: DEAV2002/0004 US NP
;   CURRENT APPLICATION NUMBER: US/10/348,081
;   CURRENT FILING DATE: 2003-01-21
;   SOFTWARE: Patentin version 3.2
; SEQ ID NO 12
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus

US-10-348-081-12

Query Match   95.0%; Score 1584; DB 4; Length 313;
Best Local Similarity 94.2%; Pred. No. 3e-134;
Matches 295; Conservative   8; Mismatches 10; Indels   0; Gaps   0;

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Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
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Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQYTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
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Db  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPSPSK 313
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RESULT 9
US-10-705-757-4
Sequence 4, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
;   APPLICANT: GRUENENTHAL GMBH
;   TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
;   FILE REFERENCE: 029310.52818US
;   CURRENT APPLICATION NUMBER: US/10/705,757
;   CURRENT FILING DATE: 2003-11-12
;   PRIOR APPLICATION NUMBER: PCT/EP02/05234
;   PRIOR FILING DATE: 2002-05-13
;   PRIOR APPLICATION NUMBER: DE 101 23 055.9
;   PRIOR FILING DATE: 2001-05-11
;   NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 4
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
;   SOFTWARE: Patentin Ver. 2.1

US-10-705-757-4

Query Match   95.0%; Score 1584; DB 4; Length 313;
Best Local Similarity 94.2%; Pred. No. 3e-134;
Matches 295; Conservative   8; Mismatches 10; Indels   0; Gaps   0;

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Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
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Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPSPSK 313
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RESULT 10
US-09-971-791-9
Sequence 9, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
;   APPLICANT: Rosanna Kapeller-Libermann
;   APPLICANT: Laura A. Rudolph-Owen
;   APPLICANT: Kyle Macbeth
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THE
;   FILE REFERENCE: 35800/2338856
;   CURRENT APPLICATION NUMBER: US/09/971,791
;   CURRENT FILING DATE: 2001-10-04
;   PRIOR APPLICATION NUMBER: 09/644,450
;   PRIOR FILING DATE: 2000-08-23
;   PRIOR APPLICATION NUMBER: 09/237,543

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;   PRIOR FILING DATE: 1999-01-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 9
;   TYPE: PRT
;   LENGTH: 313
;   ORGANISM: Homo sapiens
US-09-971-791-9

Query Match       94.8%;  Score 1582;  DB 3;  Length 313;
Best Local Similarity  93.9%;  Pred. No. 4.6e-134;
Matches  294;  Conservative  10;  Mismatches  9;  Indels  0;  Gaps  0;

Qy      1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
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Db      1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy    121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180
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Db    121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy    181  EIKLIDFGSGALLKDTVYTDFDFGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI  240
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Db    181  ELKLIDFGSGALLKDTVYTDFDFGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI  240

Qy    241  PFEHDEEIIKGQVFFRQTVSSECOHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300
           |:|||||||||||||||||||||||||||||||||||||||||||:|:||||||||||
Db    241  PFEHDEEIIRGQVFFRQRVSSECOHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy    301  EIHLHSLSPGSSK  313
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Db    301  EIHLHSLSPGPSK  313


RESULT 11
US-10-081-119-18
;  Sequence 18, Application US/10081119
;  Publication No. US2003004549IA1
;  GENERAL INFORMATION:
;  APPLICANT: Reinhard, Christoph
;  APPLICANT: Jefferson, Anne B.
;  APPLICANT: Chan, Vivien W.
;  TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
;  TITLE OF INVENTION: Target in Cancer
;  FILE REFERENCE: 16932.002
;  CURRENT APPLICATION NUMBER: US/10/081,119
;  CURRENT FILING DATE: 2002-02-21
;  PRIOR APPLICATION NUMBER: 60/289,813
;  PRIOR FILING DATE: 2001-02-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 18
;  LENGTH: 313
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-081-119-18

Query Match       94.8%;  Score 1582;  DB 4;  Length 313;
Best Local Similarity  93.9%;  Pred. No. 4.6e-134;
Matches  294;  Conservative  10;  Mismatches  9;  Indels  0;  Gaps  0;

Qy      1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
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Db      1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
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Db     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
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(Additional RESULT 12 and RESULT 13 alignment blocks continue on the right portion of the page, repeating the same sequence alignment format with similar data.)

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APPLICANT: MUELLER, Guenter
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAV2002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2
SEQ ID NO 13
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-348-081-13

Query Match         94.8%;    Score 1582;  DB 4;  Length 313;
Best Local Similarity  93.9%;    Pred. No. 4.6e-134;
Matches   294; Conservative   10; Mismatches   9;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGGSGFGSVYSGIRVAD 60
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Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          |||||||||||||||||||||| ||| |||||||||||||||||||||||||||||| ||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Qy  241 PFEHDEEIIKGQVFFRQTVSSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
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Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy  301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPGPSK 313


RESULT 14
US-10-664-421-1
Sequence 1, Application US/10664421
Publication No. US20040142864A1
GENERAL INFORMATION:
APPLICANT: BREMER, RYAN
APPLICANT: IBRAHIM, PRABHA
APPLICANT: KUMAR, ABHINAV
APPLICANT: MANDIYAN, VALSAN
APPLICANT: MILBURN, MICHAEL V.
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 03963/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 1
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-664-421-1

Query Match         94.8%;    Score 1582;  DB 4;  Length 313;
Best Local Similarity  93.9%;    Pred. No. 4.6e-134;
Matches   294; Conservative   10; Mismatches   9;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGGSGFGSVYSGIRVAD 60
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Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          |||||||||||||||||||||| ||| |||||||||||||||||||||||||||||| ||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
          |||||||| ||||||||| ||||||||| |||:|||||| |||| |||| ||  ||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy  301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPGPSK 313


RESULT 15
US-10-664-421-150
Sequence 150, Application US/10664421
Publication No. US20040142864A1
GENERAL INFORMATION:
APPLICANT: BREMER, RYAN
APPLICANT: IBRAHIM, PRABHA
APPLICANT: KUMAR, ABHINAV
APPLICANT: MANDIYAN, VALSAN
APPLICANT: MILBURN, MICHAEL V.
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 03963/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 150
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-664-421-150

Query Match         94.8%;    Score 1582;  DB 4;  Length 313;
Best Local Similarity  93.9%;    Pred. No. 4.6e-134;
Matches   294; Conservative   10; Mismatches   9;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGGSGFGSVYSGIRVAD 60
          |||||||||||||| |||||||||||||||||||||||||| | ||||||||||||:|
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          |||||||||||||||||||||| ||| |||||||||||||||||||||||||||||| ||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
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Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Qy  301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPGPSK 313
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OM protein - protein search, using sw model

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GenCore version 5.1.7

Run on: May 4, 2006, 05:27:44 ; Search time 15.3333 Seconds
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Title: 1668
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRAPCNDL..........LLPQAASEIHLHSLPGSSK 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA New:*
     1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep1:*
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     7: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
     8: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1:*
     9: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1:*
    10: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1:*
    11: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1:*
    12: /SIDS5/ptodata/2/pubpaa/US0_NEW_PUB.pep:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1122.5	67.3	455	9	US-10-784-004-373	Sequence 373, App
2	854.5	51.2	334	8	US-11-096-568A-32575	Sequence 32575, A
3	854.5	51.2	334	8	US-11-087-099-2982	Sequence 2982, Appl
4	850	51.0	311	9	US-10-501-841-32	Sequence 32, Appl
5	850	51.0	311	9	US-10-501-841-40	Sequence 40, Appl
6	379	22.7	311	11	US-11-103-065-2	Sequence 2, Appli
7	378.5	22.7	504	11	US-11-087-099-9816	Sequence 9816, Ap
8	373.5	22.4	661	8	US-10-505-928-690	Sequence 690, Appl
9	371.5	22.3	256	11	US-10-877-346-74	Sequence 74, Appl
10	371.5	22.3	256	11	US-10-877-346-72	Sequence 72, Appl
11	370	22.2	256	11	US-11-113-424-183	Sequence 183, Appl
12	362.5	21.7	514	11	US-11-087-099-11500	Sequence 11500, A
13	361	21.6	950	9	US-10-501-035-357	Sequence 357, App
14	359.5	21.6	513	11	US-11-087-099-11726	Sequence 11726, A
15	357	21.4	631	11	US-11-241-056-11	Sequence 11, Appl
16	357	21.4	512	11	US-11-087-099-3997	Sequence 3997, Ap
17	356	21.3	514	11	US-11-087-099-11838	Sequence 11838, A
18	351.5	21.1	472	11	US-11-087-099-12331	Sequence 12331, A
19	347	20.8	504	11	US-11-096-568A-22124	Sequence 22124, A
20	345	20.7	464	11	US-10-501-841-37	Sequence 37, Appl
21	344	20.6	86	9	US-10-784-004-435	Sequence 435, App
22	344	20.6	722	9	US-10-784-004-951	Sequence 951, App
23	342.5	20.5	445	11	US-11-096-568A-32575	Sequence 32575, A
24	342	20.5	513	11	US-11-087-099-7631	Sequence 7631, Ap
25	341.5	20.5	619	11	US-11-087-099-12402	Sequence 12402, A
26	338	20.3	1518	11	US-11-087-099-1886	Sequence 1886, Ap
27	336.5	20.2	448	11	US-11-096-568A-18364	Sequence 18364, A
28	334	20.0	651	9	US-10-770-726-67	Sequence 67, Appl
29	334	20.0	651	11	US-11-177-138-10	Sequence 10, Appl
30	333	20.0	620	11	US-11-087-099-3898	Sequence 3898, Ap
31	333	20.0	439	11	US-11-096-568A-20431	Sequence 20431, A
32	329	19.7	439	11	US-11-096-568A-20430	Sequence 20430, A
33	329	19.7	443	11	US-11-087-099-905	Sequence 905, App
34	328	19.7	765	9	US-10-204-639-65	Sequence 65, Appl
35	326.5	19.6	715	9	US-10-204-639-17	Sequence 17, Appl
36	326	19.6	689	11	US-11-087-099-8865	Sequence 8865, Ap
37	325.5	19.5	432	11	US-11-096-568A-32576	Sequence 32576, A
38	325	19.5	729	9	US-10-995-561-881	Sequence 881, App
39	325	19.5	729	9	US-10-995-561-878	Sequence 878, App
40	325	19.5	737	9	US-10-995-561-880	Sequence 880, App
41	325	19.5	744	9	US-10-995-561-876	Sequence 876, App
42	325	19.5	753	9	US-10-995-561-877	Sequence 877, App
43	324.5	19.5	358	9	US-10-979-095-6	Sequence 6, Appli
44	324.5	19.5	611	11	US-11-087-099-8358	Sequence 8358, Ap
45	324.5	19.5	706	11	US-11-087-099-4237	Sequence 4237, Ap

ALIGNMENTS

RESULT 1
US-10-784-004-373

; Sequence 373, Application US/10784004
; Publication No. US20060084066A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec
; TITLE OF INVENTION: Surrogate Markers of Pain
; FILE REFERENCE: 08201.6029-00000
; CURRENT APPLICATION NUMBER: US/10/784,004
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 1251
; SOFTWARE: Patentin version 3.2
US-10-784-004-373

; SEQ ID NO 373
; LENGTH: 455
; TYPE: PRT
; ORGANISM: rat

  Query Match   67.3%; Score 1122.5; DB 9; Length 455;
  Best Local Similarity   71.0%; Pred. No.1.9e-90;
  Matches 213; Conservative   31; Mismatches   43; Indels 13; Gaps   5;

Qy   1 MLLSKINSLAHLRAPC-----NDLHATKLAPGK-EKEPLBSQYQVGPLLGSGGFGSVYS 54
              |||| |||| | ::| |||| |||::| ::|| :||| ||:||||||:
Db   130 MLLSKFGSLAHL----CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVVA 185

Qy   55 GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112
              ||| ||||||||||||:| ||||||||||||||||||||||| ||||||||||||||||
Db   186 GSRIADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFER 244

Qy   113 PDSFVLILERPEPVQDLLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN 172
              |||::|:||||| |||||| ||:|||||| ||||| ||||||||||||||||:||||||||||
Db   245 PDGFLLVLERPEPAQDLLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDEN 304

Qy   173 ILIDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL 232
              |:|:|:|:||||||||||:||||||||||||||:|||||||||:||||||:|||||||||||
Db   305 LIVDLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPEWIRYHRYHGRSATVWSLGVLL 364

Qy   233 YDMVCGDIPFEHDEEIIKGQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQG 292
              |||:||||||||||||:|||||:|::::||: | ||:||:|||:|||||:||:||||:||||
Db   365 YDMVCGDIPFEQDEEILRGRLFRRRVSPECCQQLIEWCLSLRPSERPSLDQIAAHPWMLG 424

RESULT 2

US-10-511-937-2982
; Sequence 2982, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200010A
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3317
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2982
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2982

Query Match   51.2%; Score 854.5; DB 8; Length 334;
Best Local Similarity   59.6%; Pred. No. 3.6e-67;
Matches 164; Conservative 39; Mismatches 67; Indels   5; Gaps   2;

Qy   28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP 87
           :|::| |||||| ||::| | |::||:||| ||::|: ::|::|||||||||||
Db   22 GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPNRVLGWSPLSDSVTCP 81

Qy   88 MEVVLLKKVSS--DFSGVIRLLDWFERPDSFVLILEREPPVQDLFDFITERGALQEDLAR 145
           |||||||||| |||:|||||||||| |||:|:|||| ||:|||||||||||||||||
Db   82 LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141

Qy   146 GFFWQVLEAVRHCHNCGVLHRDIKDENILLIDLSRGEIKLIDFGSGALLKDTVYTDFDGTR 205
           |||||||||||||||||||||||||||||||||||||||||:||||||||:||:|||||||
Db   142 CFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSSGALLHDEPYTDFDGTR 201

Qy   206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIKGQVFFRQTVSSECQH 265
           ||||||| ||:|| ||||||||||||||||||||||||:|||||:||||:|||||||:|
Db   202 VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA 261

Qy   266 LIKWCLSLRPSDRPSFEEIRNHPWMQ---GDLLPQ 297
           ||::| :||||:|||||||||||||| |||||
Db   262 LIRRCLAPKPSSRPSLEEILLDPWMQTPAEDVTPQ 296

RESULT 3
US-10-501-841-32
; Sequence 32, Application US/10501841
; Publication No. US20060084055A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
; TITLE OF INVENTION: and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058-014402PC

; CURRENT APPLICATION NUMBER: US/10/501,841
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-841-32

Query Match   51.2%; Score 854.5; DB 9; Length 334;
Best Local Similarity   59.6%; Pred. No. 3.6e-67;
Matches 164; Conservative 39; Mismatches 67; Indels   5; Gaps   2;

Qy   28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP 87
           :|::| |||||| ||::| | |::||:||| ||::|: ::|::|||||||||||
Db   22 GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPNRVLGWSPLSDSVTCP 81

Qy   88 MEVVLLKKVSS--DFSGVIRLLDWFERPDSFVLILEREPPVQDLFDFITERGALQEDLAR 145
           |||||||||| |||:|||||||||| |||:|:|||| ||:|||||||||||||||||
Db   82 LEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141

Qy   146 GFFWQVLEAVRHCHNCGVLHRDIKDENILLIDLSRGEIKLIDFGSGALLKDTVYTDFDGTR 205
           |||||||||||||||||||||||||||||||||||||||||:||||||||:||:|||||||
Db   142 CFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSSGALLHDEPYTDFDGTR 201

Qy   206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIKGQVFFRQTVSSECQH 265
           ||||||| ||:|| ||||||||||||||||||||||||:|||||:||||:|||||||:|
Db   202 VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA 261

Qy   266 LIKWCLSLRPSDRPSFEEIRNHPWMQ---GDLLPQ 297
           ||::| :||||:|||||||||||||| |||||
Db   262 LIRRCLAPKPSSRPSLEEILLDPWMQTPAEDVTPQ 296

RESULT 4
US-10-501-841-40
; Sequence 40, Application US/10501841
; Publication No. US20060084055A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
; TITLE OF INVENTION: and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058-014402PC
; CURRENT APPLICATION NUMBER: US/10/501,841
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-841-40

Query Match   51.0%; Score 850; DB 9; Length 311;
Best Local Similarity   60.5%; Pred. No. 8.2e-67;
Matches 161; Conservative 38; Mismatches 65; Indels   2; Gaps   1;

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RESULT 5
US-11-103-065-2
; Sequence 2, Application US/11103065
; Publication No. US20050282189A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel E. Lora, Jose M.
; TITLE OF INVENTION: 2150, Human Protein Kinase Family
; TITLE OF INVENTION: Member and Uses Therefor
; FILE REFERENCE: MPI2001-137P1RNM
; CURRENT APPLICATION NUMBER: US/11/103,065
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: US/10/184,563
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,702
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-103-065-2

Query Match      51.0%;  Score 850; DB 11;  Length 311;
Best Local Similarity   60.5%;  Pred. No. 8.2e-67;
Matches   161;  Conservative  38;  Mismatches  65;  Indels  2;  Gaps  1;

Qy   28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP  87
Db   22 GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP  81

Qy   88 MEVVLLKKVSS--DFSGVIRLLDWFERPDSFVLILEREPVQDLFDFITERGALQEDLAR  145
Db   82 LEVALIWKVGAGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR  141

Qy  146 GFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIIDFGSGALLKDTVYTDFDGTR  205
Db  142 CFFGQVVAAIQHCSRGVVHRDIKDENILIDLRRGCAKLIIDFGSGALLHDEPYTDFDGTR  201

Qy  206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDIPFEHDEEIIKGQVFFRQTVSSECQH  265
Db  202 VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA  261

Qy  266 LIKWCLSLRPSDRPSFEEIRNHPWMQ  291
Db  262 LIRRCLAPKPSSRPSLEEILLDPWMQ  287


RESULT 6
US-11-087-099-9816
; Sequence 9816, Application US/11087099
; Publication No. US2006041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9816
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Cucumis sativus
US-11-087-099-9816

Query Match      22.7%;  Score 379; DB 11;  Length 504;
Best Local Similarity   35.5%;  Pred. No. 2.5e-25;
Matches   94;  Conservative  47;  Mismatches  108;  Indels  16;  Gaps  8;

Qy   38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS  97
Db    8 YKLGKTLGIGSFGKVIAEHALTGHKVAIKILNRRKIKN---LDMEEKVRREIKILRLFM  64

Qy   98 SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH  157
Db   65 HPH--IIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY  121

Qy  158 CHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFPD-GRVYSSPEWIRYH  216
Db  122 CHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK  180

Qy  217 RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----IKGQVF-FRQTVSSECQHLKW  269
Db  181 LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELIPS  239

Qy  270 CLSLRPSDRPSFEEIRNHPWMQGDL  294
Db  240 MLVVDPMKRITIPEIRQHPWFQAHL  264


RESULT 7
US-10-505-928-690
; Sequence 690, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 690
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-690

Query Match      22.7%;  Score 378.5; DB 8;  Length 661;
Best Local Similarity   34.6%;  Pred. No. 3.9e-25;
Matches   92;  Conservative  47;  Mismatches  114;  Indels  13;  Gaps  7;

Qy   31 KEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEV  90
Db   48 KHNLKHYELQETIGKGTYGKVRATERFSGRVAIKSIRKDKIKDQDM---VHIRREI  104

Qy   91 VLLKKVSSDFSGVIRLLDWFERPDSFVLILEREPVQDLFDFITERGALQEDLARGFFWQ  150
Db  105 EIMS--SLNHHIISIYEVFENKDKIVIIMEYASK-GELYDYISERRLSERETRHFFRQ  161

Qy  151 VLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIIDFG-SGALLKDTVYTDFDGTRVYSP  209
```

Left column

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Qy

Db    162 IVSAVHYCHKNGVVHRDLKLENILLD-DNCNIKIADFGLSNLYQKDFKFLQTFCGSPLYAS 220
Qy    210 PEWIRYHRYHGRSAAVWSLGILLYDMYCGDIP---FEHDEEI--IKGQVFFRQTVSSECQ  264
Db    221 PEIVNGRPYRGPEVDSWALGVLLYTLLVYGTMPFDGFDHKNLIRQISSGEYREPTQPSDAR 280
Qy    265 HLIKWCLSLRPSDRPSFEEIRNHPWM 290
Db    281 GLIRWMLMVNPDRRATIEDIANHWWV 306
```

RESULT 8
US-10-877-346-74
; Sequence 74, Application US/10877346
; Publication No. US20060014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 74
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein kinase
; OTHER INFORMATION: domain Consensus Sequence
US-10-877-346-74

Query Match 22.4%; Score 373.5; DB 9; Length 256;
Best Local Similarity 36.6%; ;Pred. No. 3.2e-25;
Matches 97; Conservative 45; Mismatches 100; Indels 23; Gaps 10;

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Qy     38 YQVGPLLGSGGGFGSVSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
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Right column

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Db    231 DLIKKCLNCDPEKRPTAKEILNHPW 255
Qy    265 HLIKWCLSLRPSDRPSFEEIRNHPW 289
Db    172 EGRGYSSK-VDVWSLGVILYELLTGKLPFPGIDPLEELFRIKERPRLRLPLPPNCSEELK 230
Qy    214 RYHYHGRSAAVWSLGILLYDMYCGDIP---FEHDEEI--IKGQVFFRQTVSSECQ 264
Db    157 HCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVY----TDFDGTRVYSPPEWI 213
Qy    113 YLHSRGIVHRDLKPENILLD--ENGTVKIADFGLARKLESSSYEKLTTFVGTPEYMAPEVL 171
Db     98 SDFSGVIRLLDWFERPDSFVLILERPEPVQDLLFDFITERG-ALQEDLARGFFWQVLEAVR 156
Qy     56 --HPNIVRLLGVFEEDDHLYLVMEYMEG-GDLFDYLRRNGLLSEKEAKKIALQILRGLE 112
Db      1 YELGEKLGSGAFGKVYKGHKDTGEIVAIKILKKRSLSE-----KKKRFLREIQILRRLS 55
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RESULT 9
US-10-877-346-72
; Sequence 72, Application US/10877346
; Publication No. US20060014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 72
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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;  OTHER INFORMATION: Description of Artificial Sequence:
;  OTHER INFORMATION: Serine/Threonine protein kinase Consensus
;  OTHER INFORMATION: Sequence
US-10-877-346-72

Query Match         22.3%;  Score 371.5;  DB 9;  Length 256;
Best Local Similarity    34.5%;  Pred. No. 4.8e-25;
Matches   92;  Conservative  52;  Mismatches  96;  Indels  27;  Gaps  8;

Qy   38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
         |:|| |||||||||||:||| |||||         |||
Db    1 YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKEKL----KKKKRERILREIKILKKL- 55

Qy   98 SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH 157
         |||:|||||||||| |||||||||||||||||||||||||||||||||
Db   56 -DHPNIVKLYDVFEDDKLYLVMEYCEG--GDLFDLLKKRGRLSEDEARFYARQILSALEY 113

Qy  158 CHNCGVLHRDIKDENILLIDLSRGEIKLIDFGSGALLKD--TVYTDFDGTRVSPPEWIRY 215
         ||||||||||||||||:||||||||||||||||||||   |||||||||||||||||
Db  114 LHSQGIIHRDLKPENLLLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171

Qy  216 HRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIKGQVFFRQ--------------TVSSE 262
         ||:|||||||||||||||||||||||||||||||:|||
Db  172 GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL---ALFKKIGKPPPPPPPEWKISPE 228

Qy  263 CQHLIKWCLSLRPSDRPSFEEIRNHPW 289
         |||||||||||||||||||||||||
Db  229 AKDLIKLLVKDPEKRLTAEEALEHPF 255
```

```
RESULT 10
US-11-424-183
Sequence 183, Application US/11113424
Publication No. US20050260713A1
GENERAL INFORMATION:
APPLICANT: Gangolli et al.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: US/11/113,424
CURRENT FILING DATE: 2005-04-21
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR APPLICATION FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/311,590
PRIOR APPLICATION FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/257,314
PRIOR APPLICATION FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/311,613
PRIOR APPLICATION FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/315,617
PRIOR APPLICATION FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/307,506
PRIOR APPLICATION FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/322,358
PRIOR APPLICATION FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR APPLICATION FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 60/288,153
PRIOR APPLICATION FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 190
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 183
LENGTH: 256
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: consensus
OTHER INFORMATION: sequence
US-11-424-183

Query Match         22.3%;  Score 371.5;  DB 11;  Length 256;
Best Local Similarity    34.5%;  Pred. No. 4.8e-25;
Matches   92;  Conservative  52;  Mismatches  96;  Indels  27;  Gaps  8;
```

```
Qy   38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
Db    1 YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKEKL----KKKKRERILREIKILKKL- 55
Qy   98 SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH 157
Db   56 -DHPNIVKLYDVFEDDKLYLVMEYCEG--GDLFDLLKKRGRLSEDEARFYARQILSALEY 113
Qy  158 CHNCGVLHRDIKDENILLIDLSRGEIKLIDFGSGALLKD--TVYTDFDGTRVSPPEWIRY 215
Db  114 LHSQGIIHRDLKPENLLLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171
Qy  216 HRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIKGQVFFRQ--------------TVSSE 262
Db  172 GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL---ALFKKIGKPPPPPPPEWKISPE 228
Qy  263 CQHLIKWCLSLRPSDRPSFEEIRNHPW 289
Db  229 AKDLIKLLVKDPEKRLTAEEALEHPF 255
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```
RESULT 11
US-11-087-099-11500
Sequence 11500, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
SEQ ID NO 11500
LENGTH: 514
TYPE: PRT
ORGANISM: Lycopersicon esculentum
NUMBER OF SEQ ID NOS: 12464
US-11-087-099-11500

Query Match         22.2%;  Score 370;  DB 11;  Length 514;
Best Local Similarity    34.3%;  Pred. No. 1.6e-24;
Matches   91;  Conservative  50;  Mismatches 108;  Indels  16;  Gaps  8;

Qy   38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
Db   19 YKLGKTLGIGSFGRVKIAEHTLTGHKVAVKILNRRKIRN--MDMEEKVRREIKILRLFM 75
Qy   98 SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH 157
Db   76 HPH--IIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 132
Qy  158 CHNCGVLHRDIKDENILLIDLSRGEIKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH 216
Db  133 CHRNMVHRDLKPENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 191
Qy  217 RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----IKGQVF-FRQTVSSECQHLIKW 269
Db  192 LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSAGARDLIPR 250
Qy  270 CLSLRPSDRPSFEEIRNHPWMQGDL 294
Db  251 MLIVDPMKRMTIPEIRLHPWFQAHL 275
```

```
RESULT 12
US-10-501-035-357
Sequence 357, Application US/10501035
Publication No. US20060046249A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
TITLE OF INVENTION: IDENTIFICATION OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE
TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
FILE REFERENCE: D0185 PCT
```

```
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: Patentin version 3.2

; SEQ ID NO 357
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-357

Query Match             21.7%;  Score 362.5;  DB 9;  Length 950;
Best Local Similarity   31.9%;  Pred. No. 1.5e-23;
Matches  83;  Conservative  52;  Mismatches 110;  Indels  15;  Gaps   6;

Qy     38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
          ||||||||||||||||| ||||||||| |||||| | ||||||||||||||| ||| |||
Db     44 YDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQL----DAVNLEKIYREVQIMKML- 98

Qy     98 SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH 157
          | |  ||||||||||||||||||||||||||||||||||||||||| ||||||||||| |
Db     99 -DHPHIIKLYQVMETKSMLYLVTEYAKN-GEIFDYLANHGRLNESEARRKFWQILSAVDY 156

Qy    158 CHNCGVLHRDIKHDENILIDLSRGEIKLIDFGSGALLKD-TVYTDFDGTRVYSPPEWIRYH 216
          ||||||||||| ||| |||||||||||||||||||||| ||| ||||||||||||||| |
Db    157 CHGRKIVHRDLKAENLLLD-NNMNIKIADFGFGNFFKSGELLATWCGSPPYAAPEVFEGQ 215

Qy    217 RYHGRSAAVWSLGILLLYDMVCGDIPFEHD------EEIIKGQVFFRQTVSSECQHLIKWC 270
          ||||||||||||||||||||||||||||||      |||||||||||||||||||||||
Db    216 QYEGPQLDIWSMGVVLYVLVCGALPFDGPTLPILRQRVLEGRFRIPYFMSEDCEHLIRRM 275

Qy    271 LSLRPSDRPSFEEIRNHPWM 290
          ||||||||||||||||||||
Db    276 LVLDPSKRLTIAQIKEHKWM 295

RESULT 13
US-11-087-099-11726
; Sequence 11726, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11,087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11726
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-11-087-099-11726

Query Match             21.6%;  Score 361;  DB 11;  Length 513;
Best Local Similarity   34.1%;  Pred. No. 9.6e-24;
Matches  94;  Conservative  46;  Mismatches 120;  Indels  16;  Gaps   8;

Qy     28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP 87
          | |  | | |||||||||||||||||||||||||||||||||||| | ||||||||||||
Db      8 GGHSEVLKN-YNLGKTLGLGTFGDVKVAERNVTGQRVAIKILNRRKMETMEMEEKGNR-- 64

Qy     88 MEVVLLKKVSSDF--SGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLAR 145
          ||| |||||       ||||||||||||||||||||||||||||||||||||||||||||
Db     65 -EIKIMRLFIDIPHPHIRVYEVIETPKDIFVVMEYCNN-GELLDYIIENGRLQEDEAR 121

Qy    146 GFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD-GT 204
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||  |
Db    122 RIFQQILAGVEYCHRIMVVHRDLKPENLLLD-SRYNVKLADFGLSNVMRDGHFLKTSCCS 180

Qy    205 RVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFEHDE------EIIKGQVFFRQT 258
          ||||||||||||||||||||||||||||||||||||||||||      |||||||||||
Db    181 LNYAAPEIISSKLYAGPEVDVWSCGVVLYALLCGSVPFDDDNIPSLFRKIKGGTYILPSY 240

RESULT 14
US-11-241-056-11
; Sequence 11, Application US/11241056
; Publication No. US20060024807A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-US
; CURRENT APPLICATION NUMBER: US/11,241,056
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/09/980,464
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-241-056-11

Query Match             21.6%;  Score 359.5;  DB 11;  Length 631;
Best Local Similarity   31.9%;  Pred. No. 1.7e-23;
Matches  98;  Conservative  54;  Mismatches 116;  Indels  39;  Gaps  10;

Qy      7 NSLAHLRARPCNDLHATKLAPGKEKEP--------------LESQYQVGPLLGSGGF 49
          || |   |    ||  |  |    | |              ||  |||||||||||||
Db     17 SALASESARP--------------LADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTY 68

Qy     50 GSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDW 109
          |||||||||||||||||||||||||||||||||||||| |||||||| ||| |||||||
Db     69 GKVKKA-RESSGRLVAIKSIRKDKIKDEQDL---LHIRREIEIMS--SLNHPHIIAIHEV 122

Qy    110 FERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIK 169
          ||||||||||||||||||||||||||||||||||||||||||||| || || |||||| |
Db    123 FENSSKIVIVMEYASR-GDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDLK 181

Qy    170 DENILIDLSRGEIKLIDFG-SGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSL 228
          |||||||||||||||||||  |||||||||||||||||||||||||||||||||||||||
Db    182 LENILLD-ANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSL 240

Qy    229 GILLLYDMVCGDIPFE-HDEEIIKGQV----FFRQTVSSECQHLIKWCLSLRPSDRPSFEE 283
          ||| ||||||||||||  | ||||||     |||| ||||||||||||||||||||||||
Db    241 GVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED 300

Qy    284 IRNHPWM 290
          ||||| |
Db    301 VASHWWV 307

RESULT 15
US-11-087-099-3997
; Sequence 3997, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11,087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3997
; LENGTH: 512
; TYPE: PRT

Qy    259 VSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDL 294
          |||||||||||||||||||||||||||||||| |||
Db    241 LSDSARDLIPKLLNIDPMKRITHEIRVHPWFKNHL 276
```

```
; ORGANISM: Solanum tuberosum
US-11-087-099-3997

Query Match     21.4%;  Score 357;  DB 11;  Length 512;
Best Local Similarity   33.8%;  Pred. No. 2.1e-23;
Matches  91;  Conservative  53;  Mismatches 101;  Indels  24;  Gaps  10;

Qy      38 YQVGPLLGSGSGGFGGSVYSGIRVADNL-----PVAIKHVEKDRISDWGELPNGTRVPMEVVLL 93
           |::| |: |  |  | : : :   : :|  :||:| : :|: ::   :  :     | :  |:|
Db      19 YKLGKTLGIGSFGKV----KIAEHTLIGHKVAVKILNRRKIRN---MDMEEKVSREIKIL 71

Qy      94 KKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLE 153
           :  | |:  :|  :|| || :  |:|| ||:| :||::| | | | ::| :
Db      72 RLFM--HGHISRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIIS 128

Qy     154 AVRHCHNCGVLHRDIKDENILIDL.SRGEIKLIDFGSGALLKDTVYTDFD-GTRVYSPPEW 212
           | |: |  | :|||||| :| :| |: | || |  | |  || :|::||  |:|:| | |
Db     129 GVEYCHINMVVHRDLKPENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEV 187

Qy     213 IRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI------IK-GQVFFRQTVSSECQH 265
           | |:: |  |  : | | ::|:|: | |||| :|::     :|  |:|  :| :: : |
Db     188 ISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGYITLPSHLSAGARD 246

Qy     266 LIKWCLSLRPSDRPSFEEIRNHPWMQGDL 294
           || | | :|| |||  : | ::| |: |
Db     247 LIPRMLIVDPMKRMTIPEIRLHPWFQAHL 275
```

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OM protein - protein search, using sw model

Run on: May 4, 2006, 05:12:40 ; Search time 113.667 Seconds
                      (without alignments)
                      1209.902 Million cell updates/sec

Title: US-10-705-757-6
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRARPCNDL.........LLPQAASEIHLHSLSPGSSK 313
Scoring table: BLOSUM62
Searched: 2443163 seqs, 439378781 residues
Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : A_Geneseq_21:*
            1: geneseqp1900s:*
            2: geneseqp1990s:*
            3: geneseqp2000s:*
            4: geneseqp2001s:*
            5: geneseqp2002s:*
            6: geneseqp2003aa:*
            7: geneseqp2003bs:*
            8: geneseqp2004s:*
            9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	ID	Description
1	1668	100.0	313	5	ABG33015	Abg33015 Mouse pro
2	1668	100.0	313	6	AAO19790	Aao19790 Murine PI
3	1668	100.0	313	7	ABR62940	Abr62940 Mouse ser
4	1668	100.0	313	8	ADN97347	Adn97347 Murine Pi
5	1668	100.0	313	8	ADR88371	Adr88371 Mus muscu
6	1668	100.0	313	9	AEA19261	Aea19261 Mouse Pin
7	1668	100.0	313	9	AEB96041	Aeb96041 House mou
8	1662	99.6	313	9	AEA19263	Aea19263 Mouse Pin
9	1584	95.0	313	6	ABG33016	Abg33016 Rat prote
10	1584	95.0	313	6	AAO19789	Aao19789 Rat PIM1
11	1584	95.0	313	7	ABR62938	Abr62938 Rat serin
12	1584	95.0	313	9	AEB96039	Aeb96039 Norway ra
13	1582	94.8	313	5	ABP54943	Abp54943 Human Pim
14	1582	94.8	313	5	ABG33017	Abg33017 Human pro
15	1582	94.8	313	6	AAO19788	Aao19788 Human PIM
16	1582	94.8	313	6	ABU61613	Abu61613 Human PIM
17	1582	94.8	313	7	ABR62939	Abr62939 Human ser
18	1582	94.8	313	7	ADE55368	Ade55368 Human Pro
19	1582	94.8	313	7	ADF45083	Adf45083 Human kin
20	1582	94.8	313	8	ADO19690	Ado19690 Human PRO
21	1582	94.8	313	8	ADR88370	Adr88370 Human PIM
22	1582	94.8	313	8	ADP24227	Adp24227 PRO polyp
23	1582	94.8	313	8	ADT07365	Adt07365 Human pro
24	1582	94.8	313	8	ADT14636	Adt14636 human Pim
25	1582	94.8	313	9	ADY86782	Ady86782 Human Pim
26	1582	94.8	313	9	AEA89424	Aea89424 Human Pim
27	1582	94.8	313	9	AEB96037	Aeb96037 Human PIM
28	1582	94.8	313	2	AAW08139	Aaw08139 Human cyt
29	1580	94.7	313	6	AAY87959	Aay87959 Human PIM
30	1580	94.7	313	8	ADI57202	Adi57202 Human CR7
31	1580	94.1	313	8	ADN03170	Adn03170 Human PIM
32	1569	94.1	313	9	ADY85580	Ady85580 Catalytic
33	1355.5	81.3	257	2	AAY43942	Aay43942 Rat prote
34	1315	78.8	253	8	ADI57241	Adi57241 PIM1 domi
35	1215.5	72.9	254	8	ADK71853	Adk71853 Human kin
36	1175	70.4	233	8	ADT07367	Adt07367 Human pro
37	1131	67.8	323	8	ADR88376	Adr88376 Columnix
38	1123.5	67.4	326	7	AAO19792	Aao19792 Murine PI
39	1123.5	67.4	326	8	ABR62933	Abr62933 Mouse pro
40	1123.5	67.4	326	8	ADO60032	Ado60032 CRH signa
41	1123.5	67.4	326	8	ADR88375	Adr88375 Mus muscu
42	1123.5	67.4	326	9	AEB96048	Aeb96048 House mou
43	1122.5	67.3	326	5	AAO20524	Aao20524 Protein s
44	1122.5	67.3	326	6	AAO19791	Aao19791 Rat PIM3
45	1122.5	67.3	326	7	ABR62936	Abr62936 Rat prote

ALIGNMENTS

RESULT 1
ABG33015
ID   ABG33015 standard; protein; 313 AA.
XX
AC   ABG33015;
XX
DT   20-DEC-2002 (first entry)
XX
DE   Mouse protein kinase phosphorylation site.
XX
KW   HKID-1; serine/threonine kinase; cellular proliferative disorder;
KW   differentiative disorder; haematopoietic neoplastic disorder;
KW   Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML;
KW   Waldenstrom's macroglobulinaemia; WM; mouse.
OS   Mus musculus.
XX
PN   US200215120-A1.
XX
PD   22-AUG-2002.
XX
PF   04-OCT-2001; 2001US-00971791.
XX
PR   26-JAN-1999; 99US-00237543.
PR   23-AUG-2000; 2000US-00644450.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
XX
DR   WPI; 2002-712471/77.
XX
PT   Modulating levels or activity of HKID-1 polypeptides, a member of
PT   serine/threonine kinase superfamily, for treating cancer, by contacting
PT   cell expressing the polypeptide with a modulator of the polypeptide.
XX
PS   Example 3; Page 38-39; 48pp; English.
XX
CC   The invention describes a method of modulating the level or activity of
CC   human HKID-1 polypeptide, a member of serine/threonine kinase
CC   superfamily. The method involves contacting a cell expressing the
CC   polypeptide or nucleic acid with an agent to modulate the level or
CC   activity of polypeptide, or level of nucleic acid molecule. The method is
CC   useful for modulating the level or activity of HKID-1 polypeptide. The
CC   polynucleotide in a subject having or predisposed to having a disorder
CC   involving cancer. Modulating HKID-1 expression or activity is useful for
CC   therapeutic purposes, for treating cellular proliferative and/or

RESULT 2

```
ID   AAO19790 standard; protein; 313 AA.
XX
AC   AAO19790;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Murine PIM1 kinase.
XX
KW   Mouse; PIM1 kinase; PIM3 kinase; pain; analgesic.
XX
OS   Mus sp.
XX
PN   WO2002093173-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-EP005234.
XX
PR   11-MAY-2001; 2001DE-0102305S.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
PI   Weihe E, Schaefer MK;
XX
DR   WPI; 2003-120715/11.
DR   N-PSDB; AB269188.
XX
PT   Method for identifying analgesics, useful particularly for treating
PT   chronic pain, by screening compounds for interaction with PIM-1 or -3
PT   kinase, or related compounds.
XX
PS   Claim 11; Fig 1F; 97pp; German.
XX
CC   The present invention relates to a method of identifying pain-regulating
CC   compounds, involving screening candidate compounds for interaction with
CC   differentiative disorders including cancer or haematopoietic neoplastic
CC   disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
CC   leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
CC   amino acid sequence of a mouse protein kinase phosphorylation site
XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1668;  DB 5;  Length 313;
Best Local Similarity   100.0%;
Matches  313;           Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGSSK 313
         |||||||||||||
Db  301 EIHLHSLSPGSSK 313
```

RESULT 3

```
ID   ABR62940 standard; protein; 313 AA.
XX
AC   ABR62940;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Mouse serine/threonine protein kinase PIM-1.
XX
KW   Mouse; PIM-1; protein kinase; enzyme.
XX
OS   Mus musculus.
XX
PN   WO2003060130-A2.
XX
PD   24-JUL-2003.
XX
PF   20-JAN-2003; 2003WO-EP000492.
XX
PR   19-JAN-2002; 2002EP-0000140l.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Korn M, Mueller G, Schneider R, Tschank G;
XX
DR   WPI; 2003-598536/56.
XX
PT   New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
PT   agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT   treating insulin resistance or type 2 diabetes mellitus.
XX
PS   Example 2; Page 40; 40pp; English.
XX
CC   The present sequence is the protein sequence of the murine
CC   serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins
CC   are the paralogues of novel human and murine PIM-3 proteins (see ABR62932
CC   PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC   useful for treating chronic pain, particularly of neuropathic or
CC   inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC   neurodegenerative diseases). The present sequence is murine PIM1 kinase
XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1668;  DB 6;  Length 313;
Best Local Similarity   100.0%;
Matches  313;           Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGSSK 313
         |||||||||||||
Db  301 EIHLHSLSPGSSK 313
```

```
CC   and ABR62933) of the invention, which are therefore expected to be
CC   involved in cancer and cell growth regulation. PIM-3 is also involved in
CC   the development of insulin resistance and type 2 diabetes mellitus. The
CC   invention relates to the use of PIM-3 nucleic acids and proteins in:
CC   screening assays for compounds that modulate insulin resistance or type 2
CC   diabetes mellitus; detection assays for detecting insulin resistance or
CC   type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
CC   forensic biology); predictive medicine (e.g. diagnostic or prognostic
CC   assays, monitoring clinical trials, pharmacogenomics); and for the
CC   preparing a medicament for the treatment of insulin resistance or type 2
CC   diabetes mellitus
XX
SQ   Sequence 313 AA;

Qy   Query Match             100.0%;   Score 1668;   DB 7;   Length 313;
Best Local Similarity       100.0%;   Pred. No. 3.8e-158;
Matches  313;    Conservative    0;   Mismatches   0;   Indels    0;   Gaps    0;

Qy      1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLILDLSRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLILDLSRG 180

Qy    181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy    301 EIHLHSLSPGSSK 313
          |||||||||||||
Db    301 EIHLHSLSPGSSK 313

RESULT 4
ADN97347
ID   ADN97347 standard; protein; 313 AA.
XX
AC   ADN97347;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Murine Pim1 SEQ ID NO:6.
XX
KW   mouse; probasin; promoter; transgenic mouse; c-myc; prostate cancer;
KW   Pim1.
XX
OS   Mus musculus.
XX
PN   WO2004000010-A2.
XX
PD   31-DEC-2003.
XX
PF   23-JUN-2003; 2003WO-US019818.
XX
PR   21-JUN-2002; 2002US-0390692P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Sawyers CL, Ellwood-Yen KB;
XX
DR   WPI; 2004-099050/10.
XX
PT   New transgenic mouse, useful as model system for the study of prostate
```

```
PT   cancer and its progression comprising a nucleic acid construct comprising
PT   a promoter operably linked to c-myc gene encoded in prostate cells of
PT   transgenic mouse.
XX
PS   Claim 7; SEQ ID NO 7; 6pp; English.
XX
CC   The invention relates to a novel transgenic mouse whose genome comprises
CC   a nucleic acid construct comprising a promoter having a fully defined
CC   nucleotide sequence comprising 310 bp (ADN97341), where the promoter is
CC   operably linked to c-myc having a fully defined nucleotide sequence
CC   comprising 1320 bp (ADN97342) where the c-myc protein encoded is
CC   expressed in prostate cells of the transgenic mouse at detectable levels.
CC   The transgenic mouse can be used as an in vivo model system for the study
CC   of prostate cancer and its progression. It can also be used in
CC   preclinical and clinical models to test novel diagnostic and therapeutic
CC   modalities including drug therapies relevant to prostate cancer
CC   prevention and progression. The transgenic animal can also be used to
CC   identify molecular markers that can be mediators of progression.
CC   Identification of the mediators is useful since they are potential
CC   therapeutic targets. The present sequence represents murine Pim1.
XX
SQ   Sequence 313 AA;

Qy   Query Match             100.0%;   Score 1668;   DB 8;   Length 313;
Best Local Similarity       100.0%;   Pred. No. 3.8e-158;
Matches  313;    Conservative    0;   Mismatches   0;   Indels    0;   Gaps    0;

Qy      1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLILDLSRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLILDLSRG 180

Qy    181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy    301 EIHLHSLSPGSSK 313
          |||||||||||||
Db    301 EIHLHSLSPGSSK 313

RESULT 5
ADR88371
ID   ADR88371 standard; protein; 313 AA.
XX
AC   ADR88371;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Mus musculus PIM 1 protein.
XX
KW   Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW   G-protein coupled receptor; methyl transferase; ligase; PIM; mouse.
XX
OS   Mus musculus.
XX
PN   US2004171062-A1.
XX
PD   02-SEP-2004.
XX
PF   28-FEB-2003; 2003US-00377268.
```

PR   28-FEB-2002; 2002US-0360651P.
PR   16-SEP-2002; 2002US-0411398P.
PR   20-SEP-2002; 2002US-0412341P.
PR   02-JAN-2003; 2003US-0437929P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
PI   Hirth K, Milburn MV;
XX
DR   WPI; 2004-642017/62.
XX
PS   Disclosure; SEQ ID NO 10; 186pp; English.
XX
PT   The present invention relates to a method of designing a ligand binding
PT   to a target molecule. The method involves identifying as molecular
CC   scaffolds compounds binding to members of a molecular family, detecting
CC   orientation of scaffolds at a binding site of target, and synthesising
CC   ligand. The invention is useful for designing drug products and for
CC   designing ligand binding to target molecules such as nuclear hormone
CC   receptors, TNF receptors, G-protein coupled receptors, methyl
CC   transferases, ligases, etc. The present sequence is the Mus musculus PIM
CC   1 protein. This sequence is used to illustrate the method of invention.
XX
SQ   Sequence 313 AA;

Query Match   100.0%; Score 1668; DB 8; Length 313;
Best Local Similarity   100.0%; Pred. No. 3.8e-158;
Matches 313;   Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy   181 EIKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EIKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy   301 EIHLHSLSPGSSK 313
              |||||||||||||
Db   301 EIHLHSLSPGSSK 313

RESULT 6
ID   AEA19261 standard; protein; 313 AA.
XX
AC   AEA19261;
XX
DT   28-JUL-2005 (first entry)
XX
DE   Mouse Pim-1 protein amino acid sequence - SEQ ID 2.
XX
KW   artery disease; vasotropic; arteriosclerosis; antiarteriosclerotic;
KW   Pim-1.
XX
OS   Mus musculus.

XX
PN   JP2005126413-A.
XX
PD   19-MAY-2005.
XX
PF   19-AUG-2004; 2004JP-00239061.
XX
PR   02-OCT-2003; 2003JP-00344914.
PA   (SOGO) SOGO IKAGAKU KENKYUSHO KK.
PA   (KATA/) KATAKAMI N.
XX
DR   WPI; 2005-395567/37.
DR   N-PSDB; AEA19260.
XX
PT   Therapeutic agent for treating artery disease e.g., arteriosclerosis,
PT   comprises a component which inhibits the function of protein Pim-1.
XX
PS   Claim 1; SEQ ID NO 2; 25pp; Japanese.
XX
CC   The invention comprises a therapeutic agent for treating artery disease
CC   which contains a component that inhibits the function of Pim-1 protein.
CC   The therapeutic agent of the invention is useful for the treatment of
CC   arteriosclerosis. The present amino acid sequence represents a mouse Pim-
CC   1 protein of the invention.
XX
SQ   Sequence 313 AA;

Query Match   100.0%; Score 1668; DB 9; Length 313;
Best Local Similarity   100.0%; Pred. No. 3.8e-158;
Matches 313;   Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy   181 EIKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EIKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy   301 EIHLHSLSPGSSK 313
              |||||||||||||
Db   301 EIHLHSLSPGSSK 313

RESULT 7
AEB96041
ID   AEB96041 standard; protein; 313 AA.
XX
AC   AEB96041;
XX
DT   20-OCT-2005 (first entry)
XX
DE   House mouse PIM-1 serine-threonine kinase protein.
XX
KW   micturition disorder; urinary dysfunction; uropathic; gene therapy;
KW   PIM-1 protein kinase; serine-threonine kinase; enzyme.
XX
OS   Homo sapiens.
XX
PN   DE102004004894-A1.

XX
PD   18-AUG-2005.
XX
PF   30-JAN-2004; 2004DE-10004894.
XX
PR   30-JAN-2004; 2004DE-10004894.
XX
PA   (CHEF) GRUENENTHAL GMBH.
XX
PI   Christoph T;
XX
DR   WPI; 2005-556609/57.
DR   N-PSDB; AEB96040.
DR   REFSEQ; NP_032866.
XX
PS   Claim 1; Fig 1F; 37pp; German.
XX
CC   The invention relates to a novel method for identifying substances that
CC   regulate urinary incontinence and the urge to urinate. The method
CC   comprises incubating a test compound with a cell and/or cell preparation
CC   that has synthesized a specific protein of the PIM (proviral integration
CC   site) kinase family and measuring either binding of the test compound to
CC   the PIM kinase, or a functional parameter that is altered by the binding.
CC   The method of the invention demonstrates uropathic and gene therapy
CC   applications and may be useful for treatment and diagnosis of urinary
CC   incontinence and the urge to urinate. The method is based upon regulating
CC   the activity or expression of PIM kinases that are involved in bladder
CC   control. The current sequence is that of the house mouse PIM-1 serine-
CC   threonine kinase protein of the invention.
XX
SQ   Sequence 313 AA;

Query Match   100.0%; Score 1668; DB 9; Length 313;
Best Local Similarity   100.0%; Pred. No. 3.8e-158;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy 301 EIHLHSLSPGSSK 313
         |||||||||||||
Db 301 EIHLHSLSPGSSK 313

RESULT 8
AEA19263
ID   AEA19263 standard; protein; 313 AA.
XX
AC   AEA19263;
XX
DT   28-JUL-2005 (first entry)
XX

DE   Mouse Pim-1-related protein amino acid sequence - SEQ ID 4.
XX
KW   artery disease; vasotropic; arteriosclerosis; antiarteriosclerotic;
KW   Pim-1.
XX
OS   Mus musculus.
XX
PN   JP2005126413-A.
XX
PD   19-MAY-2005.
XX
PF   19-AUG-2004; 2004JP-00239061.
XX
PR   02-OCT-2003; 2003JP-00344914.
XX
PA   (SOGO-) SOGO IKAGAKU KENKYUSHO KK.
PA   (KATA/) KATAKAMI N.
XX
PI   KATAKAMI N.
XX
PT   Therapeutic agent for treating artery disease e.g., arteriosclerosis,
PT   comprises a component which inhibits the function of protein Pim-1.
XX
PS   Disclosure; SEQ ID NO 4; 25pp; Japanese.
XX
CC   The invention comprises a therapeutic agent for treating artery disease
CC   which contains a component that inhibits the function of Pim-1 protein.
CC   The therapeutic agent of the invention is useful for the treatment of
CC   arteriosclerosis. The present amino acid sequence represents a mouse Pim-
CC   1-related protein of the invention.
XX
SQ   Sequence 313 AA;

Query Match   99.6%; Score 1662; DB 9; Length 313;
Best Local Similarity   99.7%; Pred. No. 1.5e-157;
Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIMHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
         ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy 301 EIHLHSLSPGSSK 313
         |||||||||||||
Db 301 EIHLHSLSPGSSK 313

RESULT 9
ABG33016
ID   ABG33016 standard; protein; 313 AA.
XX
AC   ABG33016;
XX
DT   20-DEC-2002 (first entry)
XX
DE   Rat protein kinase phosphorylation site #2.
XX

Left column

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KW  HKID-1; serine/threonine kinase; cellular proliferative disorder;
KW  differentiative disorder; cancer; haematopoietic neoplastic disorder;
KW  Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML;
KW  Waldenstrom's macroglobulinaemia; WM; rat.
XX
OS  Rattus norvegicus.
XX
PN  US200211520-A1.
XX
PD  22-AUG-2002.
XX
PF  04-OCT-2001; 2001US-00971991.
XX
PR  26-JAN-1999; 99US-00237543.
PR  23-AUG-2000; 2000US-00644450.
XX
PA  (MILL-) MILLENNIUM PHARM INC.
XX
PI  Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
XX
PS  Example 3; Page 39-40; 48pp; English.
XX
PT  Modulating levels or activity of HKID-1 polypeptides, a member of
PT  serine/threonine kinase superfamily, for treating cancer, by contacting
PT  cell expressing the polypeptide with a modulator of the polypeptide.
XX
DR  WPI; 2002-712471/77.
XX
CC  The invention describes a method of modulating the level or activity of
CC  human HKID-1 polypeptide, a member of serine/threonine kinase
CC  superfamily. The method involves contacting a cell expressing the
CC  polypeptide or nucleic acid with an agent to modulate the level or
CC  activity of polypeptide, or level of nucleic acid molecule. The method is
CC  useful for modulating the level or activity of HKID-1 polypeptide or
CC  polynucleotide in a subject having or predisposed to having a disorder
CC  involving cancer. Modulating HKID-1 expression or activity is useful for
CC  therapeutic purposes, for treating cellular proliferative and/or
CC  differentiative disorders including cancer or haematopoietic neoplastic
CC  disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
CC  leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
CC  amino acid sequence of a rat protein kinase phosphorylation site
XX
SQ  Sequence 313 AA;

Query Match    95.0%;  Score 1584;  DB 5;  Length 313;
Best Local Similarity   94.2%;
Matches 295;  Conservative  8;  Mismatches  10;  Indels  0;  Gaps  0;

Qy    1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60
         ||||||||||||| || ||||||||| |||||||||||||||||||||||||||||||||
Db    1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120
         |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180
         |||||||||||||||||||||:|||.||||||||||||||||||||||||||||||| ||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy  181  EIKLIDFGSGALLKDTVYTDFDFDGTRVYSPPEWIRYHYRHGRSAAVWSLGILLYDMVCGDI  240
         |:||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHYRHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIIKGQVFFRQYFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300
         |||||||:||::||||||    ||||||||||:||||||||||||||||:|||||| ||||| :
Db  241  PFEHDEEIVKGQYYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300

Qy  301  EIHLHSLSPGSSSK  313
         ||||||||| |||| ||
Db  301  EIHLHSLSPSPSK  313
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Right column

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RESULT 10
AA019789
ID  AA019789 standard; protein; 313 AA.
XX
AC  AA019789;
XX
DT  11-AUG-2003  (first entry)
XX
DE  Rat PIM1 kinase.
XX
OS  Rattus sp.
XX
PN  WO20029173-A2.
XX
PD  21-NOV-2002.
XX
PF  13-MAY-2002;  2002WO-EP005234.
XX
PR  11-MAY-2001;  2001DE-01023055.
XX
PA  (CHEF ) GRUENENTHAL GMBH.
XX
PI  Weihe E, Schaefer MK;
XX
PT  Method for identifying analgesics, useful particularly for treating
PT  chronic pain, by screening compounds for interaction with PIM-1 or -3
PT  kinase, or related compounds.
XX
PS  Claim 1; Fig 1D; 97pp; German.
XX
DR  WPI; 2003-120715/11.
DR  N-PSDB; AB269187.
XX
CC  The present invention relates to a method of identifying pain-regulating
CC  compounds, involving screening candidate compounds for interaction with
CC  PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC  useful for treating chronic pain, particularly of neuropathic or
CC  inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC  neurodegenerative diseases). The present sequence is rat PIM1 kinase
XX
SQ  Sequence 313 AA;

Query Match    95.0%;  Score 1584;  DB 6;  Length 313;
Best Local Similarity   94.2%;
Matches 295;  Conservative  8;  Mismatches  10;  Indels  0;  Gaps  0;

Qy    1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60
         ||||||||||||| || ||||||||| |||||||||||||||||||||||||||||||||
Db    1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120
         |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180
         |||||||||||||||||||||:|||.||||||||||||||||||||||||||||||| ||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy  181  EIKLIDFGSGALLKDTVYTDFDFDGTRVYSPPEWIRYHYRHGRSAAVWSLGILLYDMVCGDI  240
         |:||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHYRHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIIKGQVFFRQYFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300
         |||||||:||::||||||    ||||||||||:||||||||||||||||:|||||| ||||| :
Db  241  PFEHDEEIVKGQYYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300

Qy  301  EIHLHSLSPGSSSK  313
         ||||||||| |||| ||
Db  301  EIHLHSLSPSPSK  313
```

RESULT 11
ABR62938
ID   ABR62938 standard; protein; 313 AA.
XX
AC   ABR62938;
XX
DT   04-DEC-2003 (first entry)
XX
DE   Rat serine/threonine protein kinase PIM-1.
XX
KW   Rat; PIM-1; protein kinase; enzyme.
XX
OS   Rattus norvegicus.
XX
PN   WO200306O130-A2.
XX
PD   24-JUL-2003.
XX
PF   20-JAN-2003; 2003WO-EP000492.
XX
PR   19-JAN-2002; 2002EP-00001401.
XX
PA   (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI   Korn M, Mueller G, Schneider R, Tschank G;
XX
DR   WPI; 2003-598536/56.
XX
PT   New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
PT   agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT   treating insulin resistance or type 2 diabetes mellitus.
XX
PS   Example 2; Page 39; 40pp; English.
XX
CC   The present sequence is the protein sequence of the rat serine/threonine
CC   protein kinase and proto-oncogene, PIM-1. PIM-1 proteins are the
CC   paralogues of novel human and murine PIM-3 proteins (see ABR62932 and
CC   ABR62933) of the invention, which are therefore expected to be involved
CC   in cancer and cell growth regulation. PIM-3 is also involved in the
CC   development of insulin resistance and type 2 diabetes mellitus. The
CC   invention relates to the use of PIM-3 nucleic acids and proteins in:
CC   screening assays for compounds that modulate insulin resistance or type 2
CC   diabetes mellitus; detection assays for detecting insulin resistance or
CC   type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
CC   forensic biology); predictive medicine (e.g. diagnostic or prognostic
CC   assays, monitoring clinical trials, pharmacogenomics); and for the
CC   preparing a medicament for the treatment of insulin resistance or type 2
CC   diabetes mellitus
XX
SQ   Sequence 313 AA;

Query Match   95.0%; Score 1584; DB 7; Length 313;
Best Local Similarity   94.2%;
Matches 295; Conservative   8; Pred. No. 9.9e-150; Mismatches 10; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
            |||||||||||||||:|||||||:|||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
            ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
            |||||||||||||||||||||::|||:|||||||||||||||||||||||||||||||:|
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
            |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQTVSSECQHLIRWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
            |||||||||||||||||||||||||||||||||||||||||||||:|||||| ::|||||:
Db   241 PFEHDEEIVKGQVYFRQTVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy   301 EIHLHSLSPGSSK 313
            ||||||||| |||
Db   301 EIHLHSLSPSPSK 313

RESULT 12
AEB96039
ID   AEB96039 standard; protein; 313 AA.
XX
AC   AEB96039;
XX
DT   20-OCT-2005 (first entry)
XX
DE   Norway rat PIM-1 serine-threonine kinase protein.
XX
KW   micturition disorder; urinary dysfunction; uropathic; gene therapy;
KW   PIM-1 protein kinase; serine-threonine kinase; enzyme.
XX
OS   Rattus norvegicus.
XX
PN   DE102004004894-A1.
XX
PD   18-AUG-2005.
XX
PF   30-JAN-2004; 2004DE-10004894.
XX
PR   30-JAN-2004; 2004DE-10004894.
XX
PA   (CHEF) GRUENENTHAL GMBH.
XX
PI   Christoph T;
XX
DR   WPI; 2005-556609/57.
DR   N-PSDB; AEB96038.
DR   REFSEQ; NP_058730.
XX
PT   Identifying substances that regulate PIM kinases, useful for treatment
PT   and diagnosis of urinary incontinence and the urge to urinate, and
PT   similar use of PIM proteins or nucleic acids.
XX
PS   Claim 1; Fig 1D; 37pp; German.
XX
CC   The invention relates to a novel method for identifying substances that
CC   regulate urinary incontinence and the urge to urinate. The method
CC   comprises incubating a test compound with a cell and/or cell preparation
CC   that has synthesized a specific protein of the PIM (proviral integration
CC   site) kinase family and measuring either binding of the test compound to
CC   the PIM kinase, or a functional parameter that is altered by the binding.
CC   The method of the invention demonstrates uropathic and gene therapy
CC   applications and may be useful for treatment and diagnosis of urinary
CC   incontinence and the urge to urinate. The method is based upon regulating
CC   the activity or expression of PIM kinases that are involved in bladder
CC   control. The current sequence is that of the Norway rat PIM-1 serine-
CC   threonine kinase protein of the invention.
XX
SQ   Sequence 313 AA;

Query Match   95.0%; Score 1584; DB 9; Length 313;
Best Local Similarity   94.2%;
Matches 295; Conservative   8; Pred. No. 9.9e-150; Mismatches 10; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
            |||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
            ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
            |||||||||||||||||||||::|||:|||||||||||||||||||||||||||||||:|
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Db   241 PFEHDEEIVKGQVYFRQTVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy   301 EIHLHSLSPGSSK 313
            ||||||||| |||
Db   301 EIHLHSLSPSPSK 313

Db

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILLIDLNRG 180

Qy 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240

Qy 241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy 301 EIHLHSLSPGSSK 313

Db

Qy 301 EIHLHSLSPGSSK 313

Db

RESULT 13

ID   ABP54943   standard; protein; 313 AA.
AC   ABP54943;
XX
DT   13-JAN-2003 (first entry)
XX
DE   Human Pim1.
XX
KW   Pim1; tyrosine threonine kinase; TTK; protein kinase; enzyme;
KW   mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
KW   human; gene therapy.
XX
OS   Homo sapiens.
XX
XX
PN   WO200268444-A1.
XX
PD   06-SEP-2002.
XX
PF   21-FEB-2002; 2002WO-US005278.
XX
PR   21-FEB-2001; 2001US-0271254P.
XX
PA   (CHIR) CHIRON CORP.
XX
PI   Reinhard C, Jefferson AB, Chan VW;
XX
PT   Disclosure; Page 80-81; 113pp; English.
XX
PS   Reducing growth of cancer cells comprises reducing Tyrosine Threonine
PT   Kinase (TTK) activity, useful in diagnosing and treating disorders with
PT   prostate and ovarian cancer.
XX
PT   The present sequence is the protein sequence of human Pim1, a protein
CC   related to tyrosine threonine kinase (TTK, see ABP54938). TTK
CC   polynucleotides and polypeptides of the invention encompass
CC   polynucleotides and polypeptides having sequence similarity or sequence
CC   identity to human TTK and other genes and gene products related to TTK,
CC   such as Pim1. The invention is based on the finding that TTK is
CC   differentially expressed in various forms of cancer. It provides methods
CC   for the identification of cancerous cells, especially breast cancer and
CC   colon cancer cells, by detection of expression levels of TTK, as well as
CC   diagnostic, prognostic and therapeutic methods. These methods can be used
CC   as the basis of rational therapy. Assays for identifying molecules that
CC   modulate the activity of these genes in cancers, as well as methods of
CC   inhibiting tumour growth by inhibiting the activity of TTK are also
CC   provided.
XX
SQ   Sequence 313 AA;

Query Match   94.8%; Score 1582; DB 5; Length 313;
Best Local Similarity   93.9%; Pred. No. 1.6e-149;
Matches 294; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVAD 60
        :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILLIDLSRG 180
        ||||||||||||||||||| ||||:|||||||||||||||||||||||||||||||:||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILLIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240
        |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240

Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        |||||||| |||||||:||||||||||:||||:|||||||:||||:||||||:||||: :
Db 241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy 301 EIHLHSLSPGSSK 313
        |||||||||| ||
Db 301 EIHLHSLSPPSK 313

RESULT 14

ID   ABG33017   standard; protein; 313 AA.
AC   ABG33017;
XX
DT   20-DEC-2002 (first entry)
XX
DE   Human protein kinase phosphorylation site.
XX
KW   HKID-1; serine/threonine kinase; cellular proliferative disorder;
KW   differentiative disorder; cancer; haematopoietic neoplastic disorder;
KW   Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML;
KW   Waldenstrom's macroglobulinaemia; WM; human.
XX
OS   Homo sapiens.
XX
PN   US2002115120-A1.
XX
PD   22-AUG-2002.
XX
PF   04-OCT-2001; 2001US-00971791.
XX
PR   26-JAN-1999; 99US-00237543.
PR   23-AUG-2000; 2000US-00644450.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
XX
PT   WPI; 2002-712471/77.
XX
DR   WPI; 2002-712471/77.
XX
PS   Example 3; Page 40-41; 48pp; English.
XX
PT   Modulating levels or activity of HKID-1 polypeptides, a member of
PT   serine/threonine kinase superfamily, for treating cancer, by contacting
PT   cell expressing the polypeptide with a modulator of the polypeptide.
XX
CC   The invention describes a method of modulating the level or activity of
CC   human HKID-1 polypeptide, a member of serine/threonine kinase
CC   superfamily. The method involves contacting a cell expressing the
CC   polypeptide or nucleic acid with an agent to modulate the level or
CC   activity of polypeptide, or level of nucleic acid molecule. The method is
CC   useful for modulating the level or activity of HKID-1 polypeptide or
CC   polynucleotide in a subject having or predisposed to having a disorder
CC   involving cancer. Modulating HKID-1 expression or activity is useful for
CC   therapeutic purposes, for treating cellular proliferative and/or

CC   differentiate disorders including cancer or haematopoietic neoplastic
CC   disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
CC   leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
CC   amino acid sequence of a human protein kinase phosphorylation site
XX
SQ   Sequence 313 AA;

Query Match   94.8%;   Score 1582;   DB 5;   Length 313;
Best Local Similarity   93.9%;   Pred. No. 1.6e-149;
Matches 294;   Conservative 10;   Mismatches 9;   Indels 0;   Gaps 0;

```
Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
        |||||||||||||||||||||||:||||||||||||||||||||||||||||||||:|
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 EIKLIDFGSGALLKDTVTYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVTYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
        |||||||||:||||||||:|||||||||:||||:|||||||:||||||:||||||:||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGSSK 313
        |||||||||||
Db 301 EIHLHSLSPGPSK 313
```

RESULT 15
AAO19788

ID   AAO19788 standard; protein; 313 AA.
XX
AC   AAO19788;
XX
DT   11-AUG-2003 (first entry)
XX
DE   Human PIM1 kinase.
XX
KW   Human; PIM1 kinase; PIM3 kinase; pain; analgesic.
XX
OS   Homo sapiens.
XX
PN   WO2029173-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-EP005234.
XX
PR   11-MAY-2001; 2001DE-01023055.
XX
PA   (CHEF) GRUENENTHAL GMBH.
XX
PI   Weihe E, Schaefer MK;
XX
DR   WPI; 2003-120715/11.
DR   N-PSDB; ABZ69186.
XX
PT   Method for identifying analgesics, useful particularly for treating
PT   chronic pain, by screening compounds for interaction with PIM-1 or -3
PT   kinase, or related compounds.
XX
PS   Claim 1; Fig 1B; 97pp; German.
XX
CC   The present invention relates to a method of identifying pain-regulating
CC   compounds, involving screening candidate compounds for interaction with

CC   PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC   useful for treating chronic pain, particularly of neuropathic or
CC   inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC   neurodegenerative diseases). The present sequence is human PIM1 kinase
XX
SQ   Sequence 313 AA;

Query Match   94.8%;   Score 1582;   DB 6;   Length 313;
Best Local Similarity   93.9%;   Pred. No. 1.6e-149;
Matches 294;   Conservative 10;   Mismatches 9;   Indels 0;   Gaps 0;

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Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
        |||||||||||||||||||||||:||||||||||||||||||||||||||||||||:|
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 EIKLIDFGSGALLKDTVTYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVTYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
        |||||||||:||||||||:|||||||||:||||:|||||||:||||||:||||||:||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGSSK 313
        |||||||||||
Db 301 EIHLHSLSPGPSK 313
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Search completed: May 4, 2006, 05:24:46
Job time : 114.667 secs

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OM protein - protein search, using sw model
Copyright (c) 1993 - 2006 Bioacceleration Ltd.
GenCore version 5.1.7

Run on: May 4, 2006, 05:19:22 ; Search time 20.3333 Seconds
                 1481.107 Million cell updates/sec
                 (without alignments)

Title: US-10-705-757-6
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRARPCNDL.........LLPQAASEIHLHSLSPGSSK 313

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 45 summaries

Database :   PIR 80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1668	100.0	313	1	TVMSP1	protein kinase (EC
2	1584	95.0	313	1	S26298	protein kinase (EC
3	1582	94.8	313	1	TVHUP1	protein kinase (EC
4	861.5	51.6	370	1	S55333	protein kinase pim
5	628	37.6	363	2	T22255	hypothetical prote
6	504	30.2	409	2	T15435	hypothetical prote
7	391.5	23.5	481	2	I49072	protein kinase - m
8	379	22.7	504	2	T10449	probable serine/th
9	379	22.7	504	2	S66730	hypothetical prote
10	373	22.4	1101	2	JC1446	serine/threonine-s
11	373	22.4	512	2	T13741	hypothetical prote
12	372	22.3	1398	2	S33653	serine/threonine p
13	370	22.2	1358	2	A56009	serine/threonine-s
14	367	22.0	512	2	T52633	serine/threonine-s
15	361	21.6	513	2	S60304	serine/threonine-s
16	360.5	21.6	469	2	B84644	probable protein k
17	358.5	21.5	798	2	JC7500	qik protein - chic
18	357	21.4	512	2	T07788	probable serine/th
19	356	21.3	472	2	B90100	SNF1-related kinase
20	353.5	21.2	887	2	T02941	hypothetical prote
21	352	21.1	651	2	S55244	probable serine/th
22	351.5	21.1	504	2	T07415	probable serine/th
23	344.5	20.7	414	2	JN0323	Ca2+/calmodulin-de
24	344	20.6	726	2	T33998	hypothetical prote
25	342.5	20.5	445	2	T50802	serine/threonine p
26	342	20.5	502	2	T03306	hypothetical prote
27	342	20.5	513	1	S60303	serine/threonine k
28	338	20.3	1518	2	S37928	serine/threonine-s
29	334	20.0	746	2	S62365	SNF1-related prote
30	332.5	19.9	442	2	T48203	hypothetical prote
31	332	19.9	435	2	B84707	probable protein k
32	330	19.8	461	2	T14822	probable serine/th
33	328.5	19.7	1246	2	G89287	protein H39E23.1 [
34	327.5	19.6	745	2	G01025	serine/threonine p
35	327	19.6	774	2	I48609	probable serine/th
36	326.5	19.6	489	2	T04862	probable serine/th
37	326	19.5	473	2	S59941	serine/threonine-s
38	323.5	19.5	1558	2	T29253	hypothetical prote
39	323	19.4	1192	2	T29966	serine/threonine-s
40	322	19.4	713	2	S56719	probable serine/th
41	322	19.3	339	2	S44859	hypothetical prote
42	322	19.3	622	2	S27966	serine/threonine-s
43	321	19.2	423	2	T40224	protein kinase - f
44	321	19.2	552	1	A53621	[hydroxymethylglut
45	321	19.2	552	1	S51025	[hydroxymethylglut

ALIGNMENTS

RESULT 1
TVMSP1
protein kinase (EC 2.7.1.37) pim-1 - mouse
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene pro
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24169
R;Selten, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.;
Cell 46, 603-611, 1986
A;Title: The primary structure of the putative oncogene pim-1 shows extensive homology
A;Reference number: A24169; MUID:86272109; PMID:3015420
A;Accession: A24169
A;Molecule type: DNA
A;Residues: 1-313 <SEL>
A;Cross-references: UNIPROT:P06803; UNIPARC:UPI00000294AF; GB:M13945; GB:M13946; NID:g
A;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
C;Gene: pim-1
A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
A;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threo
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted

Query Match   100.0%; Score 1668; DB 1; Length 313;
Best Local Similarity 100.0%; Pred. No. 3.7e-74;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy 181 EIKLIDFGSGGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 EIKLIDFGSGGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIKGQVFRQTVSSECHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIKGQVFRQTVSSECHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy 301 EIHLHSLSPGSSK 313
         |||||||||||||
Db 301 EIHLHSLSPGSSK 313

```
Db     301 EIHLHSLSPGSSK 313
           ||||||||||||||
```

RESULT 2

Db   S26298

protein kinase (EC 2.7.1.37) pim-1 - rat
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S26298
R;Wingett, D.; Reeves, R.; Magnuson, N.S.
A;Title: Characterization of the testes-specific pim-1 transcript in rat.
A;Reference number: S26298; MUID:92319652; PMID:1620615
A;Journal: Nucleic Acids Res. 20, 3183-3189, 1992
A;Accession: S26298
A;Molecule type: mRNA
A;Residues: 1-313 <WIN>
A;Cross-references: UNIPROT:P26794; UNIPARC:UPI000012131AD6; EMBL:X63675; NID:g56902; PIDN
A;Experimental source: testis
A;Note: testis-specific transcript is shorter and more stable than the somatic transcri
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Note: in testis may be involved in signal transduction events of normal germ cell matu
C;Keywords: ATP; autophosphorylation; phosphoprotein; protein kinase homology
C;Superfamily: kinase-related transforming protein; protein kinase homology
F;36-290/Domain: protein kinase ATP-binding motif
F;44-52/Region: protein kinase homology <KIN>
F;67/Active site: Lys #status predicted

Query Match   95.0%; Score 1584; DB 1; Length 313;
Best Local Similarity   94.2%;
Matches   295; Conservative   8; Mismatches   10; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGDFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVYFRQYFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy   301 EIHLHSLSPGSSK 313
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Db   301 EIHLHSLSPGSSK 313
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A;Residues: 1-313 <REE>
A;Cross-references: UNIPROT:P11309; UNIPARC:UPI0000001060; GB:M27903; NID:g189958; PIDN:
R;Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.
A;Reference number: A46554
A;Molecule type: mRNA
A;Residues: 1-313 <MEE>
A;Cross-references: UNIPARC:UPI0000001060; GB:M24779; NID:g1065790; PIDN:AAA81553.1; PID
J. Cell. Biochem. 35, 105-112, 1987
A;Title: Cloning and characterization of the human PIM-1 gene: a putative oncogene relat
A;Accession: A46554
A;Reference number: A46554; MUID:88115604; PMID:3429489
R;Zakut-Houri, R.; Hazum, S.; Givol, D.; Telerman, A.
A;Title: The cDNA sequence and gene analysis of the human pim oncogene.
Gene 54, 105-111, 1987
A;Reference number: A27476; MUID:87274423; PMID:3475233
A;Accession: A27476
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-313 <ZAK>
A;Cross-references: UNIPROT:UPI000014987C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PID:
R;Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.
Oncogene Res. 1, 103-112, 1987
A;Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immunolo
A;Reference number: I58412; MUID:88217305; PMID:3329709
A;Accession: I58412
A;Molecule type: mRNA
A;Residues: 1-313 <DOM>
A;Cross-references: UNIPROT:UPI0000001060; GB:M54915; NID:g189961; PIDN:AAA36447.1; PID:
C;Genetics:
A;Gene: GDB:PIM1
A;Cross-references: GDB:119495; OMIM:164960
A;Map position: 6p21.2-6p21.2
A;Introns: 28/2; 63/3; 80/3; 203/1; 262/1

RESULT 3

Db    TVHUP1

protein kinase (EC 2.7.1.37) pim-1 - human
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JU0327; A46554; A27476; I58412
R;Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.
Gene 90, 303-307, 1990
A;Title: Primary structure of the putative human oncogene, pim-1.
A;Reference number: JU0327; MUID:90382681; PMID:2205533
A;Accession: JU0327
A;Molecule type: DNA

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; protein kinase homology
F;36-290/Domain: protein kinase ATP-binding motif
F;44-52/Region: protein kinase homology <KIN>
F;67/Active site: Lys #status predicted

Query Match             94.8%;  Score 1582;  DB 1;  Length 313;
Best Local Similarity   93.9%;
Matches   294;  Conservative   10;  Mismatches    9;  Indels    0;  Gaps    0;

```
Qy     1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGDFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          ||||||||||||||||||||||| |||:||||||||||||||||||||||||||||:||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| :
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVYFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
          ||||||||:|||||||| ::||||||:|||||||||||::|||||:|||||: ||||:
Db   241 PFEHDEEIRGQVFFRQRVSSECQHLIRWCLARRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGSSK 313
          |||||||| |||||
Db   301 EIHLHSLSPPSK 313
```

RESULT 4

Db   S55333

protein kinase pim-2 (EC 2.7.1.-) - mouse

C;Species: Mus musculus (house mouse)
C;Date: 10-Oct-1995 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S55333; A43093; B43093
R;van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; van der Gulden, H.; Allen
A;Title: Proviral tagging in E-mu-myc transgenic mice lacking the Pim-1 proto-oncogene l
EMBO J. 14, 2536-2544, 1995
A;Reference number: 1
A;Accession: S55333
A;Molecule type: mRNA
A;Residues: 1-370 <VAN>
A;Cross-references: UNIPARC:UPI00000028629; GB:L41495; NID:g765065; PIDN:
A;Note: 34K form
A;Accession: A43093
A;Molecule type: mRNA
A;Residues: 'M', 61-370 <VA3>
A;Cross-references: UNIPARC:UPI000000278BF; GB:L41495; NID:g765065; PIDN:AAA98924.1; PID:
A;Note: 37K form
A;Accession: B43093
A;Molecule type: mRNA
A;Residues: 'M', 27-370 <VA2>
A;Cross-references: UNIPARC:UPI000000278BE; GB:L41495; NID:g765065; PID:
A;Note: 40K form
A;Accession: A43093
A;Cross-references: UNIPROT:Q62070; GB:L41495; NID:g765065; PIDN:
A;Note: locus between A-raf and Act-7, near Kv4.1
A;Start codon: CTG
A;Map position: X
A;Gene: Pim-2
C;Genetics:
C;Comment: Pim-2 autophosphorylates at unknown sites.
C;Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotra
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Function:
F;89-345/Domain: protein kinase homology <KIN>
F;97-105/Region: protein kinase ATP-binding motif
F;120/Active site: Lys #status predicted

```
Query Match      51.6%;
Best Local Similarity   55.7%;  Score 861.5;  DB 1;  Length 370;
Matches 167;  Conservative 41;  Mismatches 87;  Indels 5;  Gaps 2;

Qy   12 LRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEK 71
Db   65 LQGHPSPPVTPQPPGGKDRAAFEAEYRLGPLLGKGGFGGTVFAGHRVTDRRQVAIKVISR 124

Qy   72 DRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFERRDSFVLILERPEPVQDL 129
Db  125 NRVLGWSTVSDSVTCPLEVALLWKVGEGNGHPGVIRLLDWFETPEGFMLVLERMPAQDL 184

Qy  130 FDFITERGALQEDLARGFFWQVLEAVRHCNCGVLHRDIKDENILIDLSRGEIKLIDFGS 189
Db  185 FDYITEKGPLGESCSRSFFTQVVAAVQHCHARGVVHRDIKDENILIDLCRGSIKLIDFGS 244

Qy  190 GALLKDTVYTFDPGTRVSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEII 249
Db  245 GALLHDEPYTDFDGTRVSPPEWISRHQYHALPATVWSLGVLLYDMVCGDIPFERDQEIL 304

Qy  250 KGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAASEIIHSLSP 309
Db  305 EAELHFPAHVSPDCCALIRRCLAPKPCSRPSLEEILLDPWMQS---PAEEKPINSSKGSP 361
```

RESULT 5
T22255
hypothetical protein F45H7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T22255
R;Percy, C.
submitted to the EMBL Data Library, June 1994
A;Reference number: Z19538
A;Accession: T22255
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:Q20443; UNIPARC:UPI0000175SA4; EMBL:Z34800; PIDN:CAA84323.
A;Experimental source: clone F45H7
C;Genetics:
A;Map position: 3
A;Introns: 72/3; 160/3; 310/1
C;Superfamily: protein kinase homology

```
Query Match      37.8%;
Best Local Similarity   46.0%;  Score 628;  DB 2;  Length 363;
Matches 122;  Conservative 48;  Mismatches 89;  Indels 6;  Gaps 3;

Qy   35 ESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLK 94
Db   28 KKNYKLKAELGRGGFGGVVYRAVRTCDNALVAVKFIERSNVKEWARI-NGEQVPMEICMLA 86

Qy   95 KVSSDFSGVIRLLDWFERRDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEA 154
Db   87 KCSK-VRGVIRLLDWYSIPEGFLIVWERPYPCIDMPDFIKGQGKISEDMARFLFRQIAVT 145

Qy  155 VRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTFDPGTRVSPPEWIR 214
Db  146 VHECVQNRVLHRDLKDENIVIDLVTGSTKLIDFGAATVLRRSQYSDFQGTRLYCPEWFL 205

Qy  215 YHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI----IKGQVFFRQTVSSECQHLIKWC 270
Db  206 HSLYLGREAAVWSLGVLIYNSLNGRLPFRNEKDICTAHLLGPLPFFVPVSAEVKDLISKC 265

Qy  271 LSLRPSDRPSFEEIRNHPWMQGDLL 295
Db  266 LTFDPQRCSLEAILNHPWVKQQTL 290
```

RESULT 6
T15435
hypothetical protein C06E8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15435
R;Favello, A.
submitted to the EMBL Data Library, February 1994
A;Description: The sequence of C. elegans cosmid C06E8.
A;Reference number: 218350
A;Accession: T15435
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-409 <FAV>
A;Cross-references: UNIPARC:UPI000017B744; EMBL:U00034; NID:g458983; PID:g458986; PIDN
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C06E8.3
A;Introns: 24/1; 76/3; 107/2; 145/3; 199/1; 307/1; 375/1

```
Query Match      30.2%;
Best Local Similarity   36.9%;  Score 504;  DB 2;  Length 409;
Matches 109;  Conservative 54;  Mismatches 124;  Indels 8;  Gaps 5;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
Db    1 MIKRKLQDLAVCCSYQVDFLHEKK----HSVKEFKRKYEVLDEIGRGGFGIVYEATTRQD 56

Qy   61 -NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLI 119
Db   57 GQQPVAVKFVQHKHVRSW-TMTCRQLIPSEVCHL-ETCEDIPGVIKILDWFANSKGFLIV 114

Qy  120 LEREPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHN-CGVLHRDIKDENILIDLS 178
Db  115 MERPANCMDLFDMVSVHGPLNEDMGKFIFKQVITVVFNMYSKHGLLHRDIKDENLIVNMN 174

Qy  179 RGEIKLIDFGSSGALLKDTVYTFDPGTRVSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG 238
Db  175 TGEVKLVDFGATAYAEKATKKEFQGTRSYCPPEWRDQLYLPLEATSWSLGVLFLLTG 234
```

```
RESULT 7

Qy    239 DIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPMQGD 293
          ::||::|||||||||||||||||||||||||||||||||||||||||||||
Db    235 KLPFRNEIQICLGNVKFPPDLSKEVCQLVKSCLTTSTSARASLAQIAAHPWMETD 289

I49072
protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Accession: I49072
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
R;Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
A;Title: Identification of novel protein kinases expressed in the myocardium of the deve
Mech. Dev. 48, 153-164, 1994
A;Reference number: I49071; MUID:95200798; PMID:7893599
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-481 <RES>
A;Cross-references: UNIPARC:UPI000017A422; EMBL:U11494; NID:g595420; PIDN:AAA67926.1; PI
C;Keywords: ATP
F;71-324/Domain: protein kinase homology <KIN>
F;79-87/Region: protein kinase ATP-binding motif

Query Match             23.5%;  Score 391.5; DB 2;  Length 481;
Best Local Similarity   33.5%;  Pred. No. 2e-12;
Matches   104; Conservative   55; Mismatches 126; Indels  25; Gaps  11;

Qy      4 SKINSLAHLRARP----------CNDLHATKLAPGKEKEPLE-SQYQVGPLLGSSGGFGSV-YSGI 56
          :|: :|  |              :|| | :::|     ||:  ::|: |||||| | ||| :|
Db     33 SRVGSRRAAEVRPEAMVIMSEFRAVPSGTGRSQKPLRVGFYDVERTLGKGNFAVVKLRGH 92

Qy     57 RVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSF 116
          ||||:| |||||||||||||||||||||||||||||||| | :| :| |||| ||| | |
Db     93 RVT-KTQVAIKIIDKTRL----DSSNLEKIYREVQLMKLL--NHPNIIKLYQVMETKDML 145

Qy    117 VLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILID 176
          || |:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    146 YIVTEFAKN-GEMEDYLTSNGHLSENEARQKFWQILSAVEYCHNHHIVHRDLKTENLLLD 204

Qy    177 LSRGEIKLIDFGSGALLK-DTVYTDFDGTRVSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
          ::|||||||||||||||  ||| ||||||||||||||||||||||||||||||||||
Db    205 -SNMDIKLADFGFGNFYKPGEPLSTCVGSPPYAAPEVFEGKEYEGPQLDVWSLGVVLYVL 263

Qy    236 VCGDIPFEHD-----EEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPW 289
          :| |||| |      ||||||||||||||||||||||||||||||||||||||||||||
Db    264 VCGSLPFDGPNLPTLRQRVLEGRFRIPFFMSQDCETLIRRMLVVDPAKRITIAQIRQHRW 323

Qy    290 MQGD--LLPQ 297
          |  |   ||
Db    324 MQADPTLLQQ 333
```

```
RESULT 8

T10449
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N;Alternate names: SNF1-related protein kinase
C;Species: Cucumis sativus (cucumber)
A;Accession: T10449
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-Oct-2004
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-504 <GUM>
A;Accession: T10449
R;Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z17020
A;Accession: T10449
A;Molecule type: mRNA
A;Residues: 1-504 <GUM>
A;Cross-references: UNIPROT:P93113; UNIPARC:UPI00000A4B92; EMBL:Y10036
A;Experimental source: cv. Masterpiece; cotyledon
A;Function:
C;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: SNF1-related protein kinase; protein kinase homology
```

```
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>

Query Match             22.7%;  Score 379; DB 2;  Length 504;
Best Local Similarity   35.5%;  Pred. No. 8.3e-12;
Matches    94; Conservative   47; Mismatches 108; Indels  16; Gaps   8;

Qy     38 YQVGPLLGSSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
          |:|||||||| | ||| :||||||||||||||||||||||||||||||||||||||
Db      8 YKLGKTLGISGSFGKVRIAEHALTGHKVAIKILNRKIKN---LDMEEKVRREIKILRLFM 64

Qy     98 SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH 157
          |||||||| ||||||||: | ||| ||| |||||||||||||| |||| || |||
Db     65 HPH--IIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 121

Qy    158 CHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVSPPEWIRYH 216
          |||||||||||||||| | |||||||||||||| || | ||||||||||||||||
Db    122 CHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 180

Qy    217 RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI------IKGQVF-FRQTVSSECQHLIKW 269
          ||| || |||:|||||||: | |||||||||      |||||  |||||||||||||||
Db    181 LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELIPS 239

Qy    270 CLSLRPSDRPSFEEIRNHPMMQGDL 294
          :  ||||||||||||||||||||
Db    240 MLVVDPMKRITIPEIRQHPMFQAHL 264
```

```
RESULT 9

S66730
hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2034
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Oct-2004
A;Accession: S66730
R;Ansorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wiemann, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66723
A;Accession: S66730
A;Molecule type: DNA
A;Accession: S66730
A;Residues: 1-1101 <ANS>
A;Cross-references: UNIPROT:Q08217; UNIPARC:UPI00012DF35; EMBL:Z74788; NID:g1419846; PI
A;Experimental source: strain S288C
C;Genetics:
A;Cross-references: SGD:S0005405
A;Map position: 15L
C;Keywords: ATP
A;Accession: S66730
F;839-1099/Domain: protein kinase homology <KIN>
F;847-855/Region: protein kinase ATP-binding motif

Query Match             22.7%;  Score 379; DB 2;  Length 1101;
Best Local Similarity   33.5%;  Pred. No. 1.6e-11;
Matches    91; Conservative   60; Mismatches  95; Indels  26; Gaps   8;

Qy     36 SQYQVGPLLGSSGGFGSVYSGIRVADNLPVAIKHVEKDRI--SDW-----GELPNGTRVP 87
          |: |:||||||||| | ||| :|||||||||||||||||  ||      |||||||||
Db    839 SDFIILQVMGEGAYGKVNLCIHNREHYIVVIKMIFKERILVDTWVRDRKLGTIPSEIQI- 897

Qy     88 MEVVLLKKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQ-----DLFDFITERGALQE 141
          ||||||||| |||  |||||||||||||| || ||| ||     ||||||||||||
Db    898 --MATLNKNSQE--NILKLLDFFEDDDYYI----ETPVHGETGSIDLFDVIEFKKDMVE 949

Qy    142 DLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDF 201
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    950 HEAKLVFKQVVASIKHLHDQGIVRHDIKDENIVD-SHGFVKLIDFGSAAYIKSGPFDVF 1008

Qy    202 DGTRVSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIKGQVFFRQT-V 259
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||  :
Db   1009 VGTMDYAAPEVLGGSSYKGKPQDIWALGVLLYTIIYKENPYYNIDEILEGELRFDKSEHV 1068

Qy    260 SSECQHLIKWCLSLRPSDRPSFEEIRNHPMMQ 291
          |::| |||||||||||||||||||||||||
Db   1069 SEECISLIKILTREVDKDRPTIDEIYEDKWLK 1100
```

```
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>
```

RESULT 10
JC1446
N;Alternate names: protein kinase SNF1 homolog
serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Oct-2004
C;Accession: JC1446; S58266; S66334
R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
Gene 120, 249-254, 1992
A;Reference number:
A;Accession: JC1446; MUID:93013041; PMID:1339973
A;Molecule type: DNA
A;Residues: 1-512 <LEG>
A;Cross-references: UNIPROT:Q38997; UNIPARC:UPI000012DE43; GB:M93023; NID:g166599; PID:
R;Thuemler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase g
Plant Mol. Biol. 29, 551-565, 1995
A;Reference number: S66314; MUID:96123233; PMID:8534852
A;Accession: S66334
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 144-198 <THU>
A;Cross-references: UNIPARC:UPI00000DEE0; EMBL:X86966; NID:g928909; PID:CAA60529.1; PI
A;Accession: S58266
A;Reference number: S58256
A;Residues: 144-198 <TH2>
A;Cross-references: UNIPARC:UPI00000DEE0; EMBL:X86966; NID:g928909; PID:CAA60529.1; PI
A;Description: Differential accumulation of the transcripts of 22 novel protein kinase g
submitted to the EMBL Data Library, May 1995
C;Comment: This enzyme plays an important role in a signal transduction cascade regulati
C;Genetics:
C;Gene: AKin10; AK21
C;Keywords: ATP; magnesium; phosphotransferase; protein kinase homology; serine/threonine-specific protein kinase
C;Superfamily: SNF1-related protein kinase; protein kinase homology <KIN>
C;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
F;Function:
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
A;Residues:
A;Intons: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3

Query Match 22.4%; Score 373; DB 1; Length 512;
Best Local Similarity 34.7%; Pred. No. 1.6e-11;
Matches 94; Conservative 47; Mismatches 114; Indels 16; Gaps 8;

```
Qy   32 EPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV 91
Db   13 ESILPNYKLGRTLGIGSFGRVKIAEHALTGHKVAVKILNRRKIKN---MEMEEKVRREIK 69

Qy   92 LLKKVSSDFSGVIRLLDWFERPDSFVLILERPEVQDLFDFITERGALQEDLARGFFMQV 151
Db   70 IIRLFMHPH--IIRLYEVIETPTDIYLVMEYVNS-GELFDYIVEKGRLQEDEARNFFQQI 126

Qy  152 LEAVRHCHCNGGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD-GTRVSPP 210
Db  127 ISGVEYCHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAP 185

Qy  211 EWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI------IKGQVF-PRQTVSSEC 263
Db  186 EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSPGA 244

Qy  264 QHLIKWCLSLRPSDRPSFEEIRNHPWMQGDL 294
Db  245 RDLIPRMLVVDPMKRVTIPEIRQHPWFQAHL 275
```

RESULT 11

T13741
hypothetical protein 2285.8 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13741
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
R;Reference number: 217668
A;Accession: T13741
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1398 <MUR>
A;Cross-references: UNIPROT:O77268; UNIPARC:UPI0000820A3; EMBL:AL031765; NID:e1371523
C;Genetics:
A;Cross-references: FlyBase:FBgn0006667
A;Note: EG:2285.8

Query Match 22.4%; Score 373; DB 2; Length 1398;
Best Local Similarity 32.6%; Pred. No. 3.8e-11;
Matches 90; Conservative 59; Mismatches 109; Indels 18; Gaps 9;

```
Qy   29 KEKEPLE-SQYQVGPLLGSGGFGSV-YSGIRVADNLPVAIKHVEKDRISDWGELPNGTRV 86
Db  131 KLKEPMRVGFYDIERTIGKGNFAAVVKLARRHRITKN-EVAIKIIDKSQL---DQTNLQKV 185

Qy   87 PMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLILERPEVQDLFDFITERGALQEDLARG 146
Db  186 YREVEIMKRLKHPH--IIKLYQVMETKNMIYIVSEYASQ-GEIFDYIAKYGRMSESAARF 242

Qy  147 FFWQVLEAVRHCHCNGGVLHRDENILIDLSRGEIKLIDFG-SGALLKDTVYTDFDGTR 205
Db  243 KFWQIISAVEYCHKKGIVHRDLKAENLLLDINM-NIKIADFGFSNHFKPGEBLLATWCGSP 301

Qy  206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEIKGQVFPRQTV 259
Db  302 PYAAPEVFEGKQYTGPEIDIWSLGVVLYVLVCGALPFDDGSTLQSLRDRVLSGRFRIPFFM 361

Qy  260 SSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLL 295
Db  362 SSECHLIRRMLVLEPTRRYTIDQIKRHRWMCPELL 397
```

RESULT 12
S33653
probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisia
N;Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 02-Aug-1994 #text_change 05-Oct-2004
C;Accession: S33653; S36717; S36732; JH0486
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.; Barton, A.; Kab
Yeast 9, 543-549, 1993
A;Reference number: S33653; MUID:93311122; PMID:8322517
A;Accession: S33653
A;Molecule type: nucleic acid sequence not shown
R;Ouellette, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N
A;Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae en
submitted to the EMBL Data Library, January 1993
A;Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a
A;Reference number: S36711
A;Accession: S36717
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-1358 <CLA>
A;Cross-references: UNIPROT:P31374; UNIPARC:UPI000017A449; EMBL:L05146
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N
Yeast 8, 133-145, 1992
A;Reference number: S22266; MUID:92221690; PMID:1561836
A;Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcriptio
A;Accession: S36732
A;Residues: 867-1358 <OUE>
A;Cross-references: UNIPARC:UPI000052EA6; EMBL:L05146; NID:g1718851; PID:AAC04940.1; P
A;Residues: 1-864, 867-1358 <CLA>
A;Molecule type: DNA
A;Accession: S36711

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-862 <CL2>
A;Cross-references: UNIPARC:UPI000017A44A; EMBL:S93805
R;Sidhu, R.S.; Mathews, S.; Bollon, A.P.
Gene 107, 111-118, 1991
A;Title: Selection of secretory protein-encoding genes by fusion with PHO5 in Saccharomy
A;Reference number: JH0483; MUID:92077420; PMID:1743509
A;Accession: JH0486
A;Molecule type: DNA
A;Cross-references: UNIPARC:UPI000017A44B
A;Gene: SGD:FUN31;
C;Genetics:
A;Cross-references: SGD:S0000015; MIPS:YAL017w
A;Gene: SGD:FUN31. SSP138
A;Map position: 1L
C;Keywords: ATP; glycoprotein; phosphotransferase; serine/threonine-specific protein kin
C;Function: protein kinase homology <KIN>
F;1104-1112/Region: protein kinase ATP-binding motif
F;8,128/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1232/Active site: Asp #status predicted

Query Match
Best Local Similarity 22.3%;   Score 372;   DB 2;   Length 1358;
Matches 88; Conservative 54; Mismatches 100; Indels 16; Gaps 6;

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Qy   44 LGSGGFGSVYSGIRVADNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLLKKVS-SDF 100
Db 1104 MGEAYGKVNLCIHKKNRYIVIKMIFKERILVDTWVRDRKLGTIPSEIQIMATLNKKPH   1163

Qy  101 SGVIRLLDWFERDSFVLILEREPEVQ-------DLFDFITERGALQEDLARGFFWQVLEA  154
Db 1164 ENIRLLDFFEDDYYYI---ETPVHGETGCIDLFDLIEFKTNMTEFAKLIFKQVVAG     1219

Qy  155 VRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSSGALLKDTVYTDFDGTRVYSPPEWIR 214
Db 1220 IKHLHDQGIVHRDIKDENIVD-SKGFVKIIDFGSSAAYKSGPEDVFVGTIDYAAPEVLG   1278

Qy  215 YHYRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIKGQVFFR--QTVSSECQHLIKWCLS 272
Db 1279 GNPYEGQPQDIWAIGILLYTVVFKENPFVNIDEILEGDLKFNNAEEVSEDCIELIKSILN  1338

Qy  273 LRPSDRPSPEEIRNHPWM 290
Db 1339 RCVPKRPTIDDINNDKWL 1356
```

RESULT 13
A56009
A;Description: serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
A;Accession: A56009
A;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 05-Oct-2004
R;Muranaka, T.; Banno, H.; Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A;Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces cer
ase of Saccharomyces cerevisiae.
A;Reference number: A56009; MUID:94217693; PMID:8164654
A;Accession: A56009
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-511 <MUR>
A;Cross-references: UNIPROT:Q40544; UNIPARC:UPI00000AAD0C; GB:D26602; NID:g496384; PIDN:
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match
Best Local Similarity 22.2%;   Score 370;   DB 1;   Length 511;

Best Local Similarity 33.8%; Pred. No. 2.3e-11; Indels 16; Gaps 8;
Matches 93; Conservative 49; Mismatches 117;

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Qy  28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP  87
Db   9 GSSVESFLRNYKLGKTLGISFGKVKIAEHTLTGHKVAVKILNRRKIKN--MEMEEKVR    65

Qy  88 MEVVLLKKVSSDFSGVIRLLDWFERDSFVLILEREPEVQDLFDFITERGALQEDLARGF  147
Db  66 REIKILRLFMHPH--IIRLYEVVETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARKF 122

Qy 148 FWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSSGALLKDTVYTDFD-GTRV 206
Db 123 FQQIISGVEYCHRNMVVHRDLKPENLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPN   181

Qy 207 YSPPEWIRYHYRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI------IK-GQVFFRQTV 259
Db 182 YAAPEVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGMISLPSHL  240

Qy 260 SSECQHLIKWCLSLRPSDRPSPEEIRNHPWMQGDL 294
Db 241 SAGARDLIPRMLIVDPMKRMTIPEIRMHPWFQAHL 275
```

RESULT 14
T52633
A;Description: serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN11 [validated] - Arabidopsis t
N;Alternate names: SNF1 protein kinase homolog AKIN11
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 05-Oct-2004
A;Accession: T52633
R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machid
Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A;Title: Regulatory interaction of PRl1 WD protein with Arabidopsis SNF1-like protein ki
A;Reference number: Z25116; MUID:99235528; PMID:10220464
A;Accession: T52633
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-512 <BHA>
A;Cross-references: UNIPROT:P92958; UNIPARC:UPI00000AC16D; EMBL:X99279; PIDN:CAA67671.1
A;Gene: AKIN11
C;Function:
C;Genetics:
A;Experimental source: cultivar Columbia
A;Gene: AKIN11
C;Function:
A;Description: EC 2.7.1.-; serine/threonine-specific protein kinase homology
A;Description: serine/threonine-specific protein kinase AKIN11 [validated, ...
complements SNF1 mutations in yeast
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Query Match
Best Local Similarity 22.0%;   Score 367;   DB 2;   Length 512;
Matches 95; Conservative 47; Mismatches 113; Indels 16; Gaps 8;

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Qy  32 EPLESQYQVGPLLGSGGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV  91
Db  14 ESILPNYKLGKTLGISFGKVKIAEHVVTGHKVAIKILNRRKIKN---MEMEEKVRREIK    70

Qy  92 LLKKVSSDFSGVIRLLDWFERDSFVLILEREPEVQDLFDFITERGALQEDLARGFFWQV   151
Db  71 ILRLFMHPH--IIRQYEVIETTSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQI  127

Qy 152 LEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSSGALLKDTVYTDFD-GTRVYSPP 210
Db 128 ISGVEYCHRNMVVHRDLKPENLLD--SRCNIKIADFGLSNVMRDGHFLKTSCGSPNYAAP  186

Qy 211 EWIRYHYRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-----IKGQVF-FRQTVSSEC  263
Db 187 EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSEA  245

Qy 264 QHLIKWCLSLRPSDRPSPEEIRNHPWMQGDL 294
Db 246 RDLIPRMLIVDPVKRITIPEIRQHRWFQTHL 276
```

```
RESULT 15
S60304
serine/threonine-specific protein kinase (EC 2.7.1.-) BKIN12 (version 2) - barley
C;Species: Hordeum vulgare (barley)
C;Date: 19-Mar-1997 #sequence_revision 15-Aug-1997 #text_change 05-Oct-2004
C;Accession: S60304; S24579
R;Halford, N.G.; Vicente-Carbajosa, J.; Sabelli, P.A.; Shewry, P.R.; Hannappel, U.; Krei
Plant J. 2, 791-797, 1992
A;Title: Molecular analyses of a barley multigene family homologous to the yeast protein
A;Reference number: S60303; MUID:93258420; PMID:1302632
A;Accession: S60304
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-513 <HAL>
A;Cross-references: UNIPROT:Q40030; UNIPARC:UPI00000172C5D; EMBL:X65604
R;Halford, N.G.
submitted to the EMBL Data Library, April 1992
A;Reference number: S24578
A;Accession: S24579
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-61, 'A', 63-513 <HA2>
A;Cross-references: UNIPARC:UPI000000A3F6F; EMBL:X65604; NID:g18933; PIDN:CAA46554.1; PID
C;Superfamily: SNF1-related protein kinase; protein kinase homology
A;Cross-references: UNIPARC:UPI000000A3F6F; EMBL:X65604; NID:g18933; PIDN:CAA46554.1; PID
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;15-272/Domain: protein kinase homology <KIN>
F;23-31/Region: protein kinase ATP-binding motif
F;46,65,143,145/Active site: Lys, Glu, Asp, Lys #status predicted
F;148,152/Binding site: magnesium (Asn, Asp) #status predicted

Query Match             21.6%;  Score 361;  DB 1;  Length 513;
Best Local Similarity   34.1%;
Matches   94;  Conservative   46;  Mismatches 120;  Indels  16;  Gaps   8;

Qy    28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP 87
         |::  :| |  | |  || |:  ||||  |:  :  :: : |||  ||| |    |
Db     8 GGHSEVLKN-YNLGKTLGLGTFGDVKVAERNVTGQRVAIKILNRRKMETMEMEEKGNR-- 64

Qy    88 MEVVLLKKVSSDF--SGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLAR 145
         ::   :    |     | | |   | : : ::  | : ||   ||:| ||   ||
Db    65 --EIKIMRLFIDFIHPHIIRVEVIETPKDIFVVMEYCNN-GELLDYIIENGRLQEDEAR 121

Qy   146 GFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDGSGALLKDTVVTDFD-GT 204
         ::|| || :   |  || || |     |  |  || ||  |||| || :| : |
Db   122 RIFQQILAGVEYCHRIMVVHRDLKPENLLLD-SRYNVKLADFGLSNVMRDGHFLKTSCGS 180

Qy   205 RVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDE----EIIKGQVFFRQT- 258
         | |  |||  :|:::  ::  ||| ||| ||    ||:|::  ::   :|| | ||
Db   181 LNYAAPEIISSKLYAGPEVDVWSCGVVLYALLCGSVPFDDDNIPSLFRKIKGGTYILPSY 240

Qy   259 VSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDL 294
         |::  |::||| |:::||  || |   |||| |
Db   241 LSDSARDLIPKLLNIDPMKRITFHEIRVHPWFKNHL 276
```

```
                    GenCore version 5.1.7
                    Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:         May  4, 2006, 05:12:40 ; Search time 122 Seconds
                    (without alignments)
                    1810.085 Million cell updates/sec

Title:          US-10-705-757-6
Perfect score:  1668
Sequence:       1 MLLSKINSLAHLRARPCNDL..........LLPQAASEIHLHSLSPGSSK 313

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:   2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 45 summaries

Database :      UniProt_05.80:*
                1: uniprot_sprot:*
                2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1668	100.0	313	1	PIM1_MOUSE	P06803; mus musculu
2	1662	99.6	313	2	Q8CFN8_MOUSE	Q8cfn8 mus musculu
3	1584	95.0	313	1	PIM1_FELCA	Q95j0 felis silve
4	1584	95.0	313	1	PIM1_RAT	P26794 rattus norv
5	1582	94.8	313	1	PIM1_HUMAN	P11309 homo sapien
6	1582	94.8	313	2	Q5TH7_HUMAN	Q5th7 homo sapien
7	1574	94.4	313	1	PIM1_BOVIN	Q9n09 bos taurus
8	1131	67.8	323	1	PIM3_COTJA	Q9pu85 coturnix co
9	1123.1	67.4	326	1	PIM3_MOUSE	Q9pu85 mus musculu
10	1122.5	67.3	326	1	PIM3_RAT	P58750 rattus norv
11	1122.5	67.3	380	2	Q4V8M2_RAT	Q4v8m2 rattus norv
12	1119	67.1	326	2	PIM3_HUMAN	Q86v86 homo sapien
13	1113	66.7	323	2	PIM3_XENLA	Q91822 xenopus lae
14	1110	66.5	325	2	Q81X8_MOUSE	Q81x8 mus musculu
15	1087	65.2	318	2	Q6II1_XENTR	Q6iii1 xenopus tro
16	1080.5	64.8	337	2	Q5U489_XENLA	Q5u489 xenopus lae
17	1056	63.3	316	2	Q4STF0_TETNG	Q4stf0 tetraodon n
18	861.5	51.6	311	2	Q8R2P0_MOUSE	Q8r2p0 mus musculu
19	861.5	51.6	370	1	PIM2_MOUSE	Q62070 mus musculu
20	850	51.0	311	1	PIM2_HUMAN	Q9p1w9 homo sapien
21	849	50.9	310	2	Q7ZVJ5_BRARE	Q7zvj5 brachydanio
22	846	50.7	310	2	Q8JFW9_BRARE	Q8jfw9 brachydanio
23	841	50.4	310	1	PIM1_BRARE	Q9yhz5 brachydanio
24	839	50.3	310	2	Q6D152_BRARE	Q6d152 brachydanio
25	787.5	47.2	288	2	Q4TDC2_TETNG	Q4tdc2 tetraodon n
26	697.5	41.8	221	2	Q8R120_MOUSE	Q8r120 mus musculu
27	628	37.6	441	2	Q20443_CAEEL	Q20443 caenorhabdi
28	624	37.4	500	2	Q61JB7_CAEBR	Q61jb7 caenorhabdi
29	513	30.8	566	2	Q61228_CAEBR	Q61228 caenorhabdi
30	504	30.2	378	2	Q8T3F1_CAEEL	Q8t3f1 caenorhabdi
31	504	30.2	566	2	Q17737_CAEEL	Q17737 caenorhabdi

32	443	26.6	270	2	Q5SPE4_BRARE	Q5spe4 brachydanio
33	425	25.5	465	2	Q5SPF6_BRARE	Q5spf6 brachydanio
34	419	25.1	416	2	Q4RFY6_TETNG	Q4rfy6 tetraodon n
35	415.5	24.9	134	2	Q6P2J9_HUMAN	Q6p2j9 homo sapien
36	400.5	24.0	268	2	Q5SPP9_BRARE	Q5spp9 brachydanio
37	400	24.0	281	2	Q5SV44_BRARE	Q5sv44 brachydanio
38	395	23.7	1383	1	PASK_MOUSE	Q8ceE6 mus musculu
39	394	23.6	125	2	Q6Q2K5_CANFA	Q6q2k5 canis fami1
40	393	23.5	341	2	Q7PR39_ANOGA	Q7pr39 anopheles g
41	391.5	23.5	261	2	Q5SPP7_BRARE	Q5spp7 brachydanio
42	391.5	23.5	261	2	Q5SPQ2_BRARE	Q5spq2 brachydanio
43	388	23.3	1385	2	Q5PQT0_RAT	Q5pqt0 rattus norv
44	385	23.1	463	2	Q5RG24_BRARE	Q5rg24 brachydanio
45	385	23.1	465	2	Q5RG26_BRARE	Q5rg26 brachydanio

ALIGNMENTS

```
RESULT 1
PIM1_MOUSE

ID   PIM1_MOUSE              STANDARD;      PRT;   313 AA.
AC   P06803;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=Pim1; Synonyms=Pim-1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
RA   Selten G., Cuypers H.T., Boelens W., Robanus-Maandag E., Verbeek J.,
RA   Domen J., van Beveren C., Berns A.;
RT   "The primary structure of the putative oncogene pim-1 shows extensive
RT   homology with protein kinases.";
RL   Cell 46:603-611(1986).
RN   [2]
RP   INTERACTION WITH RP9.
RX   MEDLINE=20389540; PubMed=10931201;
RA   Maita H., Harada Y., Nagakubo D., Kitaura H., Ikeda M., Tamai K.,
RA   Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
RT   "PAP-1, a novel target protein of phosphorylation by Pim-1 kinase.";
RL   Eur. J. Biochem. 267:5168-5178(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- DISEASE: Frequently activated by provirus insertion in murine
CC       leukemia virus-induced T-cell lymphomas.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; M13945; AAA39930.1; -; Genomic_DNA.
DR   PIR; A24169; TVMSP1.
DR   HSSP; Q63450; 1A06.
DR   SMR; P06803; 32-308.
DR   Ensembl; ENSMUSG00000024014; Mus musculus.
DR   MGI; MGI:97584; Pim1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
```

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DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN       38    290       Protein kinase.
FT   NP_BIND      44     52       ATP (By similarity).
FT   ACT_SITE    167    167       Proton acceptor (By similarity).
FT   BINDING      67     67       ATP (By similarity).
SQ   SEQUENCE   313 AA;  35537 MW;  79F4779E9DCBDC16 CRC64;

Query Match             100.0%;  Score 1668;  DB 1;  Length 313;
Best Local Similarity   100.0%;
Matches  313;  Conservative    0;  Pred. No. 2.2e-115;  Indels    0;  Gaps    0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGSSK 313
        |||||||||||||
Db  301 EIHLHSLSPGSSK 313


RESULT 2
Q8CFN8 MOUSE
ID   Q8CFN8 MOUSE PRELIMINARY;   PRT;   313 AA.
AC   Q8CFN8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Proviral integration site 1.
GN   Name=Pim1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC042885; AAH42885.1; -; mRNA.
DR   EMBL; BC053019; AAH53019.1; -; mRNA.
DR   EMBL; BC055316; AAH55316.1; -; mRNA.
DR   SMR; Q8CFN8; 32-308.
DR   Ensembl; ENSMUSG00000024014; Mus musculus.
DR   MGI; MGI:97584; Pim1.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   313 AA;  35451 MW;  1294F16A03B7C7D7 CRC64;

Query Match             99.6%;   Score 1662;  DB 2;  Length 313;
Best Local Similarity   99.7%;
Matches  312;  Conservative    0;  Pred. No. 6.1e-115;  Indels    1;  Gaps    0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGSSK 313
        |||||||||||||
Db  301 EIHLHSLSPGSSK 313
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RESULT 3
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ID    PIM1_FELCA         STANDARD;      PRT;    313 AA.
AC    Q95LJ0;
DT    28-FEB-2003 (Rel. 41, Created)
DT    28-FEB-2003 (Rel. 41, Last sequence update)
DT    13-SEP-2005 (Rel. 48, Last annotation update)
DE    Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN    Name=PIM1;
OS    Felis silvestris catus (Cat).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC    Felinae; Felis.
OX    NCBI_TaxID=9685;
RN    [1]
RP    NUCLEOTIDE SEQUENCE.
RA    Fujino Y., Satoh H., Hisasue M., Masuda K., Ohno K., Tsujimoto H.;
RT    "The cDNA sequence of the feline pim-1 oncogene.";
RL    Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC    -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC    -!- SUBUNIT: Binds to RP9 (By similarity).
CC    -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC    -!- PTM: Autophosphorylated (By similarity).
CC    -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC        subfamily.
CC    --------------------------------------------------------------------------
CC    This Swiss-Prot entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC    the European Bioinformatics Institute. There are no restrictions on its
CC    use as long as its content is in no way modified and this statement is not
CC    removed.
CC    --------------------------------------------------------------------------
DR    EMBL; AB073748; BAB71752.1; -; mRNA.
DR    SMR; Q95LJ0; 32-308.
DR    InterPro; IPR000719; Prot_kinase.
DR    InterPro; IPR008271; Ser_thr_pkin_AS.
DR    Pfam; PF00069; Pkinase; 1.
DR    ProDom; PD000001; Prot_kinase; 1.
DR    PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR    PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR    PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW    ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW    Phosphorylation; Kinase; Proto-oncogene; Serine/threonine-protein kinase;
KW    Transferase.
FT    DOMAIN         38    290       Protein kinase.
FT    NP_BIND        44     52       ATP (By similarity).
FT    ACT_SITE      167    167       Proton acceptor (By similarity).
FT    BINDING        67     67       ATP (By similarity).
SQ    SEQUENCE   313 AA;  35686 MW;  C0BE268D633E6967 CRC64;
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Query Match   95.0%;   Score 1584; DB 1;   Length 313;
Best Local Similarity   94.2%;   Pred. No. 3.7e-109;
Matches 295;   Conservative   8;   Mismatches   10;   Indels   0;   Gaps   0;

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Qy     1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MLLSKINSLAHLRTAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLSRG 180
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||| |||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFPGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           :||||||||||||||||||||||||||||||||||||||:||||:||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
           ||||||||| |||||||||||||| ||||:|:||||||||||||||||||||||||| ;
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPSFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGSSK 313
           ||||||||||||
Db   301 EIHLHSLSPGPSK 313
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RESULT 4
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ID    PIM1_RAT           STANDARD;      PRT;    313 AA.
AC    P26794;
DT    01-AUG-1992 (Rel. 23, Created)
DT    01-AUG-1992 (Rel. 23, Last sequence update)
DT    13-SEP-2005 (Rel. 48, Last annotation update)
DE    Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN    Name=Pim1; Synonyms=Pim-1;
OS    Rattus norvegicus (Rat).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC    Muroidea; Muridae; Murinae; Rattus.
OX    NCBI_TaxID=10116;
RN    [1]
RP    NUCLEOTIDE SEQUENCE.
RC    STRAIN=Sprague-Dawley; TISSUE=Testis;
RX    MEDLINE=92319652; PubMed=1620615;
RA    Wingett D., Reeves R., Magnuson N.S.;
RT    "Characterization of the testes-specific pim-1 transcript in rat.";
RL    Nucleic Acids Res. 20:3183-3189(1992).
CC    -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC    -!- SUBUNIT: Binds to RP9 (By similarity).
CC    -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC    -!- PTM: Autophosphorylated (By similarity).
CC    -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC        subfamily.
CC    --------------------------------------------------------------------------
CC    This Swiss-Prot entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC    the European Bioinformatics Institute. There are no restrictions on its
CC    use as long as its content is in no way modified and this statement is not
CC    removed.
CC    --------------------------------------------------------------------------
DR    EMBL; X63675; CAA45214.1; -; mRNA.
DR    PIR; S26298; S26298.
DR    SMR; P26794; 32-308.
DR    Ensembl; ENSRNOG00000000529; Rattus norvegicus.
DR    RGD; 3330; Pim1.
DR    InterPro; IPR000719; Prot_kinase.
DR    InterPro; IPR008271; Ser_thr_pkin_AS.
DR    Pfam; PF00069; Pkinase; 1.
DR    ProDom; PD000001; Prot_kinase; 1.
DR    PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR    PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR    PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW    ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW    Phosphorylation; Kinase; Proto-oncogene; Serine/threonine-protein kinase;
KW    Transferase.
FT    DOMAIN         38    290       Protein kinase.
FT    NP_BIND        44     52       ATP (By similarity).
FT    ACT_SITE      167    167       Proton acceptor (By similarity).
FT    BINDING        67     67       ATP (By similarity).
SQ    SEQUENCE   313 AA;  35631 MW;  D5757DA9F1821BF9 CRC64;
```

Query Match   95.0%;   Score 1584; DB 1;   Length 313;
Best Local Similarity   94.2%;   Pred. No. 3.7e-109;
Matches 295;   Conservative   8;   Mismatches   10;   Indels   0;   Gaps   0;

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Qy     1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
```

```
Qy      121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db      121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy      181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSIGILLYDMVCGDI  240
             :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSIGILLYDMVCGDI  240

Qy      241  PFEHDEEIIKGQVFFRQRTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300

Qy      301  EIHLHSLSPGSSK  313
             |||||||||||||
Db      301  EIHLHSLSPSPSK  313
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RESULT 5

ID   PIM1_HUMAN   STANDARD;   PRT;   313 AA.
AC   P11309; Q96RG3;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=90382681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
RA   Reeves R., Spies G.A., Kiefer M., Barr P.J., Power M.;
RT   "Primary structure of the putative human oncogene, pim-1.";
RL   Gene 90:303-307(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
RA   Zakut-Houri R., Hazum S., Givol D., Telerman A.;
RT   "The cDNA sequence and gene analysis of the human pim oncogene.";
RL   Gene 54:105-111(1987).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88217305; PubMed=3329709;
RA   Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
RA   Berns A.;
RT   "Comparison of the human and mouse PIM-1 cDNAs: nucleotide sequence
RT   and immunological identification of the in vitro synthesised PIM-1
RT   protein.";
RL   Oncogene Res. 1:103-112(1987).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE OF 1-202.
RX   MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085588;
RA   Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
RA   Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
RT   "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
RT   cell lymphomas.";
RL   Nature 412:341-346(2001).
RN   [7]
RP   CHARACTERIZATION.
RX   MEDLINE=88246418; PubMed=2837645;
RA   Telerman A., Amson R., Zakut-Houri R., Givol D.;
RT   "Identification of the human pim-1 gene product as a 33-kilodalton
RT   cytoplasmic protein with tyrosine kinase activity.";
RL   Mol. Cell. Biol. 8:1498-1503(1988).
RN   [8]
RP   FUNCTION.
RX   MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
RA   Koike N., Maita H., Taira T., Ariga H., Iguchi-Ariga S.M.M.;
RT   "Identification of heterochromatin protein 1 (HP1) as a
RT   phosphorylation target by Pim-1 kinase and the effect of
RT   phosphorylation on the transcriptional repression function of HP1.";
RL   FEBS Lett. 467:17-21(2000).
RN   [9]
RP   SUBCELLULAR LOCATION.
RX   MEDLINE=22557470; PubMed=12680209;
RA   Ionov Y., Le X., Tunquist B.J., Sweetenham J., Sachs T., Ryder J.,
RA   Johnson T., Lilly M.B., Kraft A.S.;
RT   "Pim-1 protein kinase is nuclear in Burkitt's lymphoma: nuclear
RA   localization is necessary for its biologic effects.";
RL   Anticancer Res. 23:167-178(2003).
CC   -!- FUNCTION: Thought to play a role in signal transduction in blood
CC   cells. May affect the structure or silencing of chromatin by
CC   phosphorylating HP1 gamma/CBX3.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC   -!- TISSUE SPECIFICITY: Expressed primarily in cells of the
CC   hematopoietic and germ line lineages.
CC   -!- PTM: Autophosphorylated on tyrosine residues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC   WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PIM1ID261.html";
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; M27903; AAA60090.1; -; Genomic_DNA.
DR   EMBL; M16750; AAA60089.1; -; mRNA.
DR   EMBL; M54915; AAA36447.1; -; mRNA.
DR   EMBL; M24779; AAB51553.1; -; mRNA.
DR   EMBL; BC020224; AAH20224.1; -; mRNA.
DR   EMBL; AF386792; AAK70871.1; -; Genomic_DNA.
DR   PIR; JU0027; TVHUP1.
DR   PDB; 1XQZ; X-ray; A=14-313.
DR   PDB; 1XR1; X-ray; A=14-313.
DR   PDB; 1XWG; X-ray; A=1-313.
DR   PDB; 1YHS; X-ray; A=33-305.

DR   PDB; 1YI3; X-ray; A=33-305.
DR   PDB; 1YI4; X-ray; A=33-305.
DR   PDB; 2BIK; X-ray; B=1-313.
DR   PDB; 2BIL; X-ray; B=1-313.
DR   Ensembl; ENSG00000137193; Homo sapiens.
DR   HGNC; HGNC:8986; PIM1.
DR   H-InvDB; HIX0005835; -.
DR   MIM; 164960; -.
DR   GO; GO:0005737; C:cytoplasm; TAS.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR   GO; GO:0007275; P:development; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   3D-structure; ATP-binding; Kinase; Nuclear protein;
KW   Nucleotide-binding; Phosphorylation; Proto-oncogene;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   38   290   Protein kinase.
FT   NP_BIND   44   52   ATP (By similarity).
FT   ACT_SITE   167   167   Proton acceptor (By similarity).
FT   BINDING   67   67   ATP (By similarity).
FT   CONFLICT   15   15   AP -> RA (in Ref. 2).
SQ   SEQUENCE   313 AA; 35686 MW; 35BA76D3668B69A3 CRC64;

Query Match   94.8%; Score 1582; DB 1; Length 313;
Best Local Similarity   93.9%;
Matches 294; Conservative   10; Mismatches   9; Indels   0; Gaps   0;

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Qy          1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
              ||||||||||||||||||||||||:|||||||||||||||||||||||||||||||:|||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVSSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
              |||||||||||||||||||||:|||||||||||||:||||||||||:|||||| ||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGSSK 313
              |||||||| |||
Db        301 EIHLHSLSPGPSK 313
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RESULT 6
Q5T7H7_HUMAN

ID   Q5T7H7_HUMAN PRELIMINARY;   PRT;   313 AA.
AC   Q5T7H7;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Pim-1 oncogene (provial integration site 1).
GN   Name=PIM1; ORFNames=RP3-355M6.1-003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]

RP   NUCLEOTIDE SEQUENCE.
RA   Laird G.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AL353579; CAI20316.1; -; Genomic_DNA.
SMR; Q5T7H7; 32-308.
DR   Ensembl; ENSG00000137193; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   313 AA; 35686 MW; 35BA76D3668B69A3 CRC64;

Query Match   94.8%; Score 1582; DB 2; Length 313;
Best Local Similarity   93.9%;
Matches 294; Conservative   10; Mismatches   9; Indels   0; Gaps   0;

```
Qy          1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
              ||||||||||||||||||||||||:|||||||||||||||||||||||||||||||:|||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVSSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
              |||||||||||||||||||||:|||||||||||||:||||||||||:|||||| ||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGSSK 313
              |||||||| |||
Db        301 EIHLHSLSPGPSK 313
```

RESULT 7
PIM1_BOVIN

ID   PIM1_BOVIN   STANDARD;   PRT;   313 AA.
AC   Q9N0P9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21109090; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2;
RA   Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;

Left column

```
RT   "cDNA cloning, sequencing and characterization of bovine pim-1.";
RL   vet. Immunol. Immunopathol. 78:177-195(2001).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   --------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------
DR   EMBL; AF250078; AAF67200.1; -; mRNA.
DR   SMR; Q9N0P9; 32-308.
DR   HSSP; Q63450; 1A06.
DR   InterPro; IPR000719; Prot kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN       38    290       Protein kinase.
FT   NP_BIND      44     52       ATP (By similarity).
FT   ACT_SITE    167            Proton acceptor (By similarity).
FT   BINDING      67            ATP (By similarity).
SQ   SEQUENCE   313 AA;  35630 MW;  9EF40229A847AD47 CRC64;

Query Match             94.4%;  Score 1574;  DB 1;  Length 313;
Best Local Similarity   93.3%;  Pred. No. 2e-108;
Matches  292;  Conservative   12;  Mismatches    9;  Indels    0;  Gaps    0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||| ||| |||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCSDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        || ||||||||||||||||||||||||||||||||||  || || |||||| | ||||||
Db   61 NLEVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSVSSGFSGVIRLLDMWFERDPSFVLL 120

Qy  121 EREPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCNCGVLHRDIKDENILIDLSRG 180
        ||||||||||||||||||||||: ||| ||||||||||||| |||||||||||||||| | |
Db  121 EREPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHDCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVYFFRQVTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
        |||||||:||||| |||| |:||||||||||||| |||||||:|||| ||| |||||||:
Db  241 PFEHDEEIVRGQVFFRQRVSSECOHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy  301 EIHLHSLSPGSSK 313
        |||||||||||:| |
Db  301 EIHLHSLSPGPSK 313

RESULT 8
PIM3_COTJA
ID   PIM3_COTJA    STANDARD;    PRT;   323 AA.
AC   Q9PU85;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (qpim).
GN   Name=PIM3; Synonyms=PIM-3;
OS   Coturnix coturnix japonica (Japanese quail).
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Right column

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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=93934;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20180111; PubMed=10713710; DOI=10.1038/sj.onc.1203355;
RA   Eichmann A., Yuan L., Breant C., Alitalo K., Koskinen P.J.;
RT   "Developmental expression of Pim kinases suggests functions also
RT   outside of the hematopoietic system.";
RL   Oncogene 19:1215-1224(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   --------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
DR   EMBL; AJ130845; CAB62386.1; -; mRNA.
DR   HSSP; Q63450; 1A06.
DR   InterPro; IPR000719; Prot kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   InterPro; IPR002290; Ser_Thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       40    291       Protein kinase.
FT   NP_BIND      46     54       ATP (By similarity).
FT   ACT_SITE    168            Proton acceptor (By similarity).
FT   BINDING      69            ATP (By similarity).
SQ   SEQUENCE   323 AA;  36597 MW;  E2A4FA20B6F63996C CRC64;

Query Match             67.8%;  Score 1131;  DB 1;  Length 323;
Best Local Similarity   67.1%;  Pred. No. 1.3e-75;
Matches  208;  Conservative   45;  Mismatches   53;  Indels    4;  Gaps    3;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAP--GKEKEPLESQYQVGPLLGSGGFGSVYSGIRV 58
        |||||  |||||   |  :  ||| ||   |:|||| |  :|||| :|||||| ||:| ||
Db    1 MLLSKFGSLAHICSPASMDHLPVKILPPVKVEKEPFDKVYQVGSVLGSGGFGTVYAGSRT 60

Qy   59 ADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVL 118
        || |||| ||| |: : :||  : ||:||||:|||||| ||||| |:||||||||||:| :
Db   61 ADGLPVAVKHVVKERVTEWGTI-GGVMVPLEIVLLKKVGSSGFRGVIKLLDWYERPDGFLI 119

Qy  119 ILEREPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCNCGVLHRDIKDENILIDLS 178
        ::|||||:|:|||||||||:|||:| :||| |||||||||||  | :|||||||||:||:|
Db  120 VMEREPELVKDLFDFITEKGALDEDTARGFRQVLEAVRHCYGCCVVHRDIKDENLLVDLR 179

Qy  179 RGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAATVWSLGILLYDMVCG 238
        ||:| :||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db  180 TGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRATVWSLGILLYDMVCG 239

Qy  239 DIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWM-QGDLLPQ 297
        ||||| |||:| |: :|| :|:|||: :|||||||||||||||::|:| ||| :  :  :
Db  240 DIPFEQDEEILRGRLYFRRRISPECQQLIKWCLSLRPSDRPTLEQIFDHQWMHKSEVVKS 299

Qy  298 AASEIHLHSL 307
        :    |:||:
Db  300 EDCDIRLRTL 309

RESULT 9
PIM3_MOUSE
ID   PIM3_MOUSE    STANDARD;    PRT;   326 AA.
```

AC   P58750;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=Pim3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; BC017621; AAH17621.1; -; mRNA.
DR   EMBL; BC026639; AAH26639.1; -; mRNA.
DR   HSSP; Q03656; 1HOW.
DR   Ensembl; ENSMUSG00000035828; Mus musculus.
DR   MGI; MGI:1355297; Pim3.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   40   293   Protein kinase.
FT   NP_BIND   46   54   ATP (By similarity).
FT   BINDING   170   170   ATP (By similarity).
FT   ACT_SITE   170   170   Proton acceptor (By similarity).
FT   BINDING   69   69   ATP (By similarity).
SQ   SEQUENCE   326 AA; 35970 MW; DD68CBF46354B51E CRC64;

     Query Match   67.4%;
     Best Local Similarity   71.0%;
     Matches 213; Conservative   31; Mismatches   43; Indels   13; Gaps   5;

Qy   1 MLLSKINSLAHLRARPC------NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS 54
              ||||| ||||| ----- :||||||:|||:: |||:|||:|:|||||||||||
Db

Db   1 MLLSKFGSLAHL-----CGPGGVDHLPVKILQPAKADKESSFEKVYQVGAVLGSGGFGTVYA 56

Qy   55 GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112
              |:|| ||| ||:||||||||::|| |||::|| ||||||||| || |||||||||||||
Db   57 GSRIADGLPVAVKHVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFER 115

Qy   113 PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN 172
              |:||:||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db   116 PDGFLLVLERPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDEN 175

Qy   173 ILIDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL 232
              :||||:||||||||||||||||||||||||||||||||||||||:||||||||||||:|:
Db   176 LIVDLRSGELKLIDFGSGAVLKDTVVTDFDGTRVVSSPPEWIRYHRYHGRSATVWSLGVLL 235

Qy   233 YDMVCGDIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQG 292
              ||||||||||||||||:||||||||:|::|| |||||||||||||||:| | ||||:|||
Db   236 YDMVCGDIPFEQDEEILRGRLFFRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWMLG 295

RESULT 10
PIM3_RAT
ID   PIM3_RAT   STANDARD;   PRT;   326 AA.
AC   O70444;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Protein kinase
DE   KID-1) (Kinase induced by depolarization).
GN   Name=Pim3; Synonyms=Kid1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RA   Konietzko U., Kuhl D.;
RT   "Pim-3 is a member of the pim kinase family.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RC   TISSUE SPECIFICITY: Present in a number of unstimulated tissues,
RX   MEDLINE=98298176; PubMed=9632723; DOI=10.1074/jbc.273.26.16535;
RA   Feldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L.,
RA   Bazan N.G., Baudry M., Herschman H.R.;
RT   "KID-1, a protein kinase induced by depolarization in brain.";
RL   J. Biol. Chem. 273:16535-16543(1998).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- TISSUE SPECIFICITY: Present in a number of unstimulated tissues,
CC   including brain.
CC   -!- INDUCTION: By membrane depolarization or forskolin.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AF086224; AAC68900.1; ALT_INIT; mRNA.
DR   EMBL; AF057026; AAC36065.1; -; mRNA.
DR   HSSP; Q03656; 1HOW.
DR   RGD; 620462; Pim3.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR   GO; GO:0046777; P:autophosphorylation; IDA.
DR   GO; GO:0016572; P:histone phosphorylation; IDA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.

DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   40   293   Protein kinase.
FT   NP_BIND   46   54   ATP (By similarity).
FT   ACT_SITE   170   170   Proton acceptor (By similarity).
FT   BINDING   69   69   ATP (By similarity).
SQ   SEQUENCE   326 AA; 36002 MW; DD6C9BF4635F851E CRC64;

Query Match   67.3%; Score 1122.5; DB 1; Length 326;
Best Local Similarity   71.0%; Pred. No. 5.7e-75;
Matches 213; Conservative   31; Mismatches   43; Indels   13; Gaps   5;

Qy   1 MLLSKINSLAHLRARPC-----NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS 54
             |||| |:|||| :|||:|||||:|| |::||::|| |:||:||||||::
Db   1 MLLSKFGSLAHL----CGPGGVDHLPVKILQPAKADKESFEKYYQVGAVLGSGGFGTVYA 56

Qy   55 GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112
             | |||:||||||:||| :: || | | | |:||||||:|| | ::|||||||||:
Db   57 GSRIADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFER 115

Qy   113 PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN 172
             ||.|.|.|||||| |||||||||||||:| |||.||.||| ||||||||||:|||||||
Db   116 PDGFLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDEN 175

Qy   173 ILIDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL 232
             :|:||.||::|||||||||:|||||||||||||||||||||||||||||||:||||:||
Db   176 LIVDLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLL 235

Qy   233 YDMVCGDIPFEHDEEIIKGQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQG 292
             ||||||||||.|:||| :|::|| ..||.| ||| |||||||:||| ::| |||| |
Db   236 YDMVCGDIPFEQDDEEILRGRLFRPRRVSPECCQQLIEWCLSLRPSERPSLDQIAAHPWMLG 295

RESULT 11
ID   Q4V8M2_RAT   PRELIMINARY;   PRT;   380 AA.
AC   Q4V8M2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";

RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RG   NIH MGC Project;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC097317; AAH97317.1; -; mRNA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
FT   NON_TER   1   1
SQ   SEQUENCE   380 AA; 41568 MW; F82BEBE50DD71346 CRC64;

Query Match   67.3%; Score 1122.5; DB 2; Length 380;
Best Local Similarity   71.0%; Pred. No. 6.9e-75;
Matches 213; Conservative   31; Mismatches   43; Indels   13; Gaps   5;

Qy   1 MLLSKINSLAHLRARPC-----NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS 54
             |||| |:|||| :|||:|||||:|| |::||::|| |:||:||||||::
Db   55 MLLSKFGSLAHL----CGPGGVDHLPVKILQPAKADKESFEKYYQVGAVLGSGGFGTVYA 110

Qy   55 GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112
             | |||:||||||:||| :: || | | | |:||||||:|| | ::|||||||||:
Db   111 GSRIADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFER 169

Qy   113 PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN 172
             ||.|.|.|||||| |||||||||||||:| |||.||.||| ||||||||||:|||||||
Db   170 PDGFLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDEN 229

Qy   173 ILIDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL 232
             :|:||.||::|||||||||:|||||||||||||||||||||||||||||||:||||:||
Db   230 LIVDLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLL 289

Qy   233 YDMVCGDIPFEHDEEIIKGQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQG 292
             ||||||||||.|:||| :|::|| ..||.| ||| |||||||:||| ::| |||| |
Db   290 YDMVCGDIPFEQDDEEILRGRLFRPRRVSPECCQQLIEWCLSLRPSERPSLDQIAAHPWMLG 349

RESULT 12
ID   PIM3_HUMAN   STANDARD;   PRT;   326 AA.
AC   Q86V86; Q68BM2;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=PIM3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY.
RC   TISSUE=Liver;
RX   PubMed=15542001; DOI=10.1002/ijc.20719;
RA   Fujii C., Nakamoto Y., Lu P., Tsuneyama K., Popivanova B.K.,
RA   Kaneko S., Mukaida N.;
RT   "Aberrant expression of serine/threonine kinase Pim-3 in
RT   hepatocellular carcinoma development and its role in the proliferation
RT   of human hepatoma cell lines.";
RL   Int. J. Cancer 114:209-218(2005).

RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   IDENTIFICATION FROM ESTS.
RX   MEDLINE=2262943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;
RA   Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.;
RT   "Consistency checks for characterizing protein forms.";
RL   Comput. Biol. Chem. 27:29-35(2003).
CC   -!- FUNCTION: May be involved in cell cycle progression and anti-
CC   apoptosis process. Implicated in proliferation of human hepatoma
CC   cell lines.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- TISSUE SPECIFICITY: Widely expressed. No expression in colon,
CC   thymus, and small intestine. Expressed in human hepatoma cell
CC   lines but not in normal liver tissues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AB114795; BAD42438.1; -; mRNA.
DR   EMBL; BC052239; -; NOT_ANNOTATED_CDS; mRNA.
DR   Ensembl; ENSG00000198355; Homo sapiens.
DR   HGNC; HGNC:19310; PIM3.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   40   293   Protein kinase.
FT   NP_BIND   46   54   ATP (By similarity).
FT   ACT_SITE   170   170   Proton acceptor (By similarity).
FT   BINDING   69   69   ATP (By similarity).
SQ   SEQUENCE   326 AA; 35863 MW; 41FDF9DD2467A162 CRC64;

Query Match   67.1%;   Score 1119; DB 1; Length 326;
Best Local Similarity   67.9%;   Pred. No. 1e-74;
Matches 216; Conservative 35; Mismatches 53; Indels 14; Gaps   6;

Qy   1 MLLSKINSLAHLRARPC-----NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFPGSVYS 54
         ||||| |||| | | || |||| | | || || | ||||||| ||
Db   1 MLLSKFGSLAHL----CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYA 56

RESULT 13
PIM3_XENLA
ID   PIM3_XENLA   STANDARD;   PRT;   323 AA.
AC   Q91822;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Pim-1).
GN   Name=PIM3; Synonyms=PIM1;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES.
RX   MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
RA   Aebersold R., Pelech S.L.;
RA   Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M.,
RT   "Identification of the autophosphorylation sites of the Xenopus laevis
RT   Pim-1 proto-oncogene-encoded protein kinase.";
RL   J. Biol. Chem. 272:10514-10521(1997).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   -!- CAUTION: Was originally (Ref.1) called Pim-1 but seems to
CC   represent the pim-3 isoform.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; L29495; AAA85389.1; -; mRNA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   40   291   Protein kinase.
FT   NP_BIND   46   54   ATP (By similarity).
FT   ACT_SITE   168   168   Proton acceptor (By similarity).
FT   BINDING   69   69   ATP (By similarity).
FT   MOD_RES   4   4   Phosphoserine (partial).
FT   MOD_RES   190   190   Phosphoserine (by autocatalysis).

Qy   55 GIRVADNLPVAIKHIVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112
Db   57 GSRIADGLPVAVKHVVKERVTEWGSL-CGATVPLEVVLLRKVGAAGGARGVIRLLDWFER 115
Qy 113 PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN 172
Db 116 PDGFLIVLERPEPAQDLFDFITERGALDEPLARRFPAQVLAAVRHCHSCGVVHRDIKDEN 175
Qy 173 ILILDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWNSLGILL 232
Db 176 LIVDLRSGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATWSLGVLL 235
Qy 233 YDMWCGDIPFEHDEEIIKGQVFRQTVSSECHLIKWCLSLRSDRPSFEEIRNHPWMQG 292
Db 236 YDMWCGDIPFEQDEEILGRLLFRRRVSPECQQLIRWCLSLRPSERFSLDQIAAHPWMLG 295
Qy 293 -DLLPQAASEIHLHSLSP 309
Db 296 ADGGAPESCDLRLCTLDP 313

```
FT   MOD_RES        205    205    Phosphothreonine (by autocatalysis)
FT
SQ   SEQUENCE       323 AA;  36964 MW;  AB4DD61E7A99A38F CRC64;

Query Match                    Best Local Similarity   66.7%;   Score 1113;   DB 1;   Length 323;
                               Conservative   65.8%;   Pred. No. 2.9e-74;
Matches  208;                  Conservative  46;  Mismatches 56;  Indels  6;  Gaps  5;

Qy      1 MLLSKINSLAHLRARPCNDLH--ATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR 57
          ||||||||||||||||||| :: ||:||||| ::::||||||:|:||:||| :||||||
Db      1 MLLSKFGSLAHI-CNPSNMEHLPVKILQPVKVDKEPFEKVYQVGSVVASGGFGTVYSDSR 59

Qy     58 VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDRFSGVIRLLDWFERPDSFV 117
          ||:|||||||||||||| ::|||:||||:|:|:||||||:|::::|||||||||||||||:
Db     60 IADGQPVAVKHVAKERVTEWGTL-NGVVMPLEIVLLKKVPTAFRGVINLLDWYERPDAFL 118

Qy    118 LILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDL 177
          ||||:||||||||||||||||||||||||||||||||||||||||||||||||||:||:
Db    119 IVWERPEPVKDLFDYITEKGPLDEDTARGFFRQVLEAVRHCYNCGVVHRDIKDENLLVDT 178

Qy    178 SRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVC 237
          :||||||||||||||||||||||||||||||||||||||||||||||||||||:|:||
Db    179 RNGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDMVY 238

Qy    238 GDIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWM-QGDLLP 296
          ||||||:|||:|||||||||||||||||||||||||||||||||||||||||| ||||||
Db    239 GDIPFEQDEEIVRLCFRRRISTECCQQLIKWCLSLRPSDRPTLEQIFDHPWMCKCCDLVK 298

Qy    297 QAASEIHLHSLSPGSS 312
          ||||||:|||||||||
Db    299 SEDCDLRLRTIDNDSS 314
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RESULT 14
ID   Q8I1X8_MOUSE   PRELIMINARY;   PRT;   325 AA.
AC   Q8I1X8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Kid1.
GN   Name=Pim3; Synonyms=Kid1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Yu L.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AY026239; AAK16606.1; -; mRNA.
HSSP; Q03656; 1Q99.
SMR; Q8I1X8; 36-292.
MGI; MGI:1355297; Pim3.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   325 AA; 35931 MW; 77DEF8B20F41E3F4 CRC64;

Query Match   Best Local Similarity   66.5%;   Score 1110;   DB 2;   Length 325;
                               Conservative 70.7%;   Pred. No. 4.8e-74;
Matches 212;   Conservative 32; Mismatches 42; Indels 14; Gaps 6;

RESULT 15
ID   Q66I11_XENTR   PRELIMINARY;   PRT;   318 AA.
AC   Q66I11;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Pim3-prov protein.
GN   Name=pim3-prov;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; BC081340; AAH81340.1; -; mRNA.
SMR; Q66I11; 32-297.
Ensembl; ENSXETG00000009354; Xenopus tropicalis.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

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Qy      1 MLLSKINSLAHLRARPC-------NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS 54
          ||||||||||||||||        ||:|||||||| :|||||||||||||| ||||| :
Db      1 MLLSKFGSLAHL----CGPGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYA 56

Qy     55 GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112
          ||  || || :||||:|||| |||||||||:|:|:||||||:   ||| ||||||||||
Db     57 GSRIADGLPVAVKHVAKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFER 115

Qy    113 PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN 172
          ||  :||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    116 PDGFLLVLLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCNCGVVHRDIKDEN 175

Qy    173 ILIDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL 232
          :|:| |||||||||||||||||||||||||||||||||||||||||||||||::|||:||
Db    176 LIVDLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLL 235

Qy    233 YDMVCGDIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQG 292
          |||||||||||:||||:|| :|||||||||||||||||||||||||| |  ||| ||||
Db    236 YDMVCGDIPFEQDEEILGRLFPRRRVSPECQQLIEWCLSLRPSERPSLDKL-CHPWMLG 294
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DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Cell cycle; Cell division; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   318 AA;  36547 MW;  48CCF12797F01FDC CRC64;
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Query Match             65.2%;   Score 1087;   DB 2;   Length 318;
Best Local Similarity   67.1%;   Pred. No. 2.4e-72;
Matches  198;  Conservative   42;  Mismatches   47;   Indels    8;   Gaps    3;

Qy      3 LSKINSLAHLRARPCNDLHATKLAPGKE------KEPLESQYQVGPLLGSSGGFGGSVYSGIRV  58
          :|.:..|...|:          .|.:.|        |||.:||.||:.::.||.||:.||:.|:
Db      1 MSSVQVIYH---QKIHNYHLNSVFPKDDLPAVKEPFENCYQGPVIGTGGFGTVYSGVRI      57

Qy     59 ADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFEERPDSFVL  118
          ::|||:||:|:.::.: .|.|:   .|.|||:||:||||:.|:||:|||||||||||:.:
Db     58 SDKLPVAIKHVSRDRIGEMKHM-NGTLVPLEIYLLKKVSNGCRGVIRLLDDWYERPDGFII  116

Qy    119 ILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLS  178
          :|||||||||||||||||||  :.| :|||||||||:.|||||||:||||||||||||||| :||
Db    117 IMERPEPVQDLFDFITERGALGEELATNFPRQVVEAVRHCHSCDVVHRDIKDENILVDLR  176

Qy    179 RGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCG  238
          ||.|||||||||||:||:.|||||||||||||||.:|||.||||||||||||||||||||||
Db    177 TAELKLIDFGSGALLRDAVYTDFDGTRVYSPPEWIRFHKYHGRSATVWSLGILLYDMVCG  236

Qy    239 DIPFEHDEEILKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGD  293
          ||||||||||:|.||.:||||||::.|||:||||||||||||||.||||.||||||
Db    237 DIPFEHDDEILKGKIQYRCRVSRECQHLIEWCLSKRPSDRPSLEQILAHPWMSQD  291
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Search completed: May  4, 2006, 05:18:58
Job time : 123 secs
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